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Result
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Listing first 45 summaries
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2: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1982.DAT:*

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HPV E6/7 region pr
HPV E6/7 region pr
Low hazard strain
Partial nucleotide
Human papillomavir
Human papillomavir
Human papillomavir
Human papillomavir
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## ALIGNMENTS

AAQ48541 standard; DNA; 20

В₽

22-FEB-1994 (first entry)

AAQ48541;

RESULT 1
AAQ48541
ID AAQ4
XX AAQ4
AC AAQ4
XX Huma
XX Huma
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XX Synt
XX Synt
XX JP05
PF 19-4
XX UF05
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XX WF1;
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XX Disc Human papilloma virus; HPV; E6; E7; benign; malignant; probe; Disclosure; Page 13; 18pp; Japanese Detecting benign and/or malignant human papilloma virus - by detecting DNA sequence of E6 and/or E7 region of human papilloma WPI; 1993-277497/35. 19-AUG-1991; 03-AUG-1993. JP05192200-A Synthetic. HPV E6/7 region probe (TAKI ) TAKARA SHUZO CO LTD 20-AUG-1990; 90JP-0217067 91JP-0230839 88

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RESULT 3
AAS18613
ID AAS1
   RESULT 2
AAQ48565
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; Page 15; 18pp; Japanese
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               Human papillomavirus; HPV; early gene;
                                               Low hazard strain human papillomavirus (HPV) E6, PCR primer.
                                                                                   26-FEB-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Detecting benign and/or malignant human papilloma virus - by detecting DNA sequence of E6 and/or E7 region of human papilloma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1993-277497/35.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (TAKI ) TAKARA SHUZO CO LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               20-AUG-1990;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               virus; HPV;
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               E6; PCR primer;
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cells is now based on identification of a nucleotide sequence in the L1 region of the genome. Identification of 6, E7 and L1 make it possible to identify the presence of HPV virus in every stage of infection and to distinguish between virus strains having having middle/high hazard. This is the primer used to identify the E6 region of the low hazard HPV strains in infected cells, described in the method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention describes a novel method of identifying viral DNA of human papillomavirus (HFV) in cellular material collected from an individual. The method comprises extracting DNA from the cellular material, amplifying the DNA by using a polymerase, and identifying sequences complementary to sequences in the regions E (early genes) e.g. E6 and E7 of the mountain process of the free contracts of the complementary to sequences in the regions E (early genes) e.g. E6 and E7 of the mountain process of the contracts of the contract of the co
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                                                                                                                                                                                                                                     Sequence 20
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The presence of HPV in
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AAN91601 standard; DNA; 731 ВP

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TGCTAATTCGGTGCTACCTG

. Similarity 20; Conser

Conservative

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Mismatches

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Indels

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Gaps

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20;

AAN91601;

17-JUL-1990 (first entry)

Partial nucleotide sequence type 6 (HPV-6). (5<sub>′</sub> end) of human papilloma virus (HPV)

Human papilloma virus; cellular smear; benign type 6; in situ hybridisation assay, cervical wart; cervical cancer.

Human papilloma virus.

W08902934-A.

30-SEP-1988; 88WO-US03367

87US-0103979

02-OCT-1987;

(MICR-) MICROPROBE CORP

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RESULT 5
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                                                                                           WPI; 1997-145619/13
P-PSDB; AAW01808.
                                                                                                                                                                                                                                                                                                                      HPV; polyprotein; vaccine; wart; cervical cancer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                AAT59430 standard; DNA; 1107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hybridisation test for human papilloma virus in cell smears by reaction with long labelled probe specific for particular
                                                       Papilloma virus early useful for treating, e
                                                                                                                            Cox JC, Edwards SJ,
Moloney MBH, Webb EA,
                                                                                                                                                                                                   27-JUL-1995;
                                                                                                                                                                                                                           26-JUL-1996;
                                                                                                                                                                                                                                                  13-FEB-1997.
                                                                                                                                                                                                                                                                         WO9705164-A1
                                                                                                                                                                                                                                                                                              Human papillomavirus
                                                                                                                                                                                                                                                                                                                                                           Human
                                                                                                                                                                                                                                                                                                                                                                                                         AAT59430;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 731 BP; 245 A; 147 C; 159 G; 180 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              virus types, esp. for examining cervical smears
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1989-114406/15
                                Example 1; Page 22-23; 62pp; English.
                                                                                                                                                                (UYQU)
                                                                                                                                                                                                                                                                                                                                                                                  26-MAY-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        400 TGCTAATTCGGTGCTACCTG 419
                                                                                                                                                                                                                                                                                                                                                        papillomavirus 6b E6/E5a/E4 DNA cassette CSL690.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 TGCTAATTCGGTGCTACCTG 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20;
                                                                                                                                                              CSL LTD.
UNIV QUEENSLAND.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; 39pp;
                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Adams TH;
                                                                                                                                                                                                   95AU-0004439
                                                                                                                                                                                                                           96WO-AU00473
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                                                        ø
                                                                                                                                                                                                                                                                                              type
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        English.
                                                                                                                           Frazer I,
Williams
                                                                   open
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                                                                                                                                                                                                                                                                                                6
                                                        n reading frame
genital warts a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0;
                                                                                                                                                                                                                                                                                                                                                                                                                                ВP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 20;
Pred. No.
                                                                                                                              ΜĐ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                  condylomata acuminata,
                                                                                                                                       Margetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0.44;
                                                        and cervical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 10;
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                                                                                                                                         McMillan
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                                                        constructs
cancer
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DNA construct CSL690 (AAT59430) codes for an E6/E5a/E4 polyprotein (AAW01808), plus C-terminal hexahistidine tag, of human

Matches

Conservative

.0;

Mismatches

0

Indels

0;

Gaps

0;

Query Match
Best Local Similarity

100.0%;

Score Pred.

No.

DB 18; 0.47;

Length 1128;

Sequence

1128 BP; 359 A; 274 C;

240 G;

255 T; 0 other;

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RESULT 6
AAT59431
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Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     papillomavirus 6b (HPV6b). It was obtd. by Separace reading amplification of the E6, E4 and E5a genes (see also AAT59412-17) of HCV6b and their cloning into vector pSP70. The resulting E6/E5a/E4 cassette was incorporated into pGEX-STOP to allow prodn. of the HPV6b polyprotein in E. coli. The E6/E5a/E4 DNA construct, or the encoded polypeptide, can be used as a vaccine to generate a humoral and/or cellular immune response against HPV, esp. for treating genital warts and cervical cancer.
                     DNA construct CSL760 (AAT59431) codes for an E6/E7/E4 polyprotein (AAW01809) of human papillomavirus 6b (HPV6b), plus a C-terminal hexahistidine tag. It was obtd. by separate PCR amplification of the E6, E4 and E7 genes (see also AAT59412-15 and AAT59418-19) of HCV6b and their cloning into vector pSP70. The resulting E6/E7/E4 cassette was incorporated into pGEX-STOP to allow prodn. of the HPV6b polyprotein in E. coli. The E6/E7/E4 DNA construct, or the encoded polypeptide, can be used as a vaccine to generate a humoral and/or cellular immune response against HPV, esp. for treating genital warts and cervical cancer.
                                                                                                                                                                                                 Papilloma virus early open reading frame polyprotein useful for treating, e.g. genital warts and cervical
                                                                                                                                                                                                                                            P-PSDB; AAW01809.
                                                                                                                                                                                                                                                                                                 Cox JC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human papillomavirus type
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HPV; polyprotein; vaccine; wart; cervical cancer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human papillomavirus 6b E6/E7/E4 DNA cassette CSL760.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAT59431 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 1107 BP; 337 A; 268 C; 213 G; 289 T; 0 other;
                                                                                                                                                                           Example 1; Page 24-25; 62pp; English.
                                                                                                                                                                                                                                                          WPI; 1997-145619/13
                                                                                                                                                                                                                                                                                   мoloney мвн, webb
                                                                                                                                                                                                                                                                                                                                                                     27-JUL-1995;
                                                                                                                                                                                                                                                                                                                                                                                               26-JUL-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                           13-FEB-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO9705164-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       26-MAY-1997 (first entry)
                                                                                                                                                                                                                                                                                                                            (CSLC-) CSL LTD.
(UYQU ) UNIV QUEENSLAND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                     95AU-0004439
                                                                                                                                                                                                                                                                                                                                                                                                96WO-AU00473
                                                                                                                                                                                                                                                                                   SJ,
b EA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%;
                                                                                                                                                                                                                                                                                     Frazer I,
Williams
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                                                                                                                                                                                                                                                                                     Margetts MP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      condylomata acuminata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    No.
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                                                                                                                                                                                                                                                                                                   McMillan
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                                                                                                                                                                                                     constructs
cancer
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RESULT 8
AAT59450
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AAT59432
ID AAT5
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                                                                                                                                                                                                                  Query Match
Best Local S
Matches 20
                 31-MAY-1997
                                                                                                                                                                                                                                                                                                                      DNA construct CSL673 (AAT59432) codes for an E6/E7/E5a/E4 polyprotein (AAW01810) of human papillomavirus 6b (HFV6b), plus a C-terminal hexahistidine tag. It was obtd. by separate PCR amplification of the E6, E4, E5a and E7 genes (see also AAT59411-19 of HCV6b and their cloning into vector pSP70. The resulting E6/E7/E5a/E4 cassette was incorporated into pGEX-STOP to allow prodn. of the HPV6b polyprotein in E. coli. The E6/E7/E5a/E4 DNA construct, or the encoded polypeptide, can be used as a vaccine to generate a humoral and/or cellular immune response against HPV, esp. for treating and the latter of the product of the polyprotein to the polypose of the product of the polyprotein and the continuous product to generate a succine to succine to generate a succine to succine to succine to succine to succine s
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                                                AAT59450;
                                                                             AAT59450 standard;
                                                                                                                                                                                                                                                                               Sequence 1398 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 1; Page 26-28; 62pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Papilloma virus early open reading frame polyprotein constructs useful for treating, e.g. genital warts and cervical cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cox JC, Edwards SJ, Moloney MBH, Webb EA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      27-JUL-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13-FEB-1997.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cervical cancer;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human papillomavirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         26-MAY-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAT59432;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               P-PSDB; AAW01810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         polyprotein; vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                299
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                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                                            genital warts and cervical cancer.
                                                                                                                                                       TGCTAATTCGGTGCTACCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TGCTAATTCGGTGCTACCTG
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V QUEENSLAND
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                 (first
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                                                                                                                                                                                                                                                                            429 A; 330
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                                                                             DNA;
                entry)
                                                                                                                                                                                                                               100.0%;
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Williams
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6b E6/E7/E5a/E4 DNA cassette CSL673
                                                                             4770
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                                                                             ВP
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Pred. No. 0.4
0; Mismatches
                                                                                                                                                                                                                                                                              C; 283
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                                                                                                                                                                                                                                                                              356 T; 0
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                                                                                                                                                                                                                                               18;
                                                                                                                                                                                                                  0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         McMillan
                                                                                                                                                                                                                                                                               other;
                                                                                                                                                                                                                                                 Length 1398;
                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                  0
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                                                                                                                                                                                                                  0;
                                                             Query Match
Best Local S
Matches 20
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A DNA construct (AAT59450) in vector pTrcHisA codes for an E2/E4/E5a/E5b/E6/E7/E1 polyprotein (AAW01816) of human papillomaviru 6 (HPV6); plus an N-terminal hexahistidine tag. It was obtd. by amplification of the individual early genes (see also AAT59436-49) and their cloning into pTrcHisA. The DNA construct, or the encoded polyprotein, can be used as a vaccine to generate a humoral and/or cellular immune response against HPV, esp. for treating genital
                                                                                                                                                                                                                                                                                                                                                                                                 mRNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human
                                                                                                                             Papilloma virus early open reading frame polyprotein useful for treating, e.g. genital warts and cervical
                                                                                                                                                                  P-PSDB;
                                                                                                                                                                                                                  Cox JC,
                                                                                                                                                                                                                                                                                                                                                  W09705164-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human papillomavirus type
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HPV; polyprotein;
cervical cancer;
                                                                                                        Example 6; Page 35-40; 62pp; English
                                                                                                                                                                                                    Moloney MBH, Webb
                                                                                                                                                                                                                                      (CSLC-) CSL LTD.
(UYQU ) UNIV QUEENSLAND
                                                                                                                                                                                                                                                                           27-JUL-1995;
                                                                                                                                                                                                                                                                                                 26-JUL-1996;
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                                                                                                                                                                  1997-145619/13.
DB; AAW01816.
 and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                papillomavirus 6 polyprotein
                                                                                                                                                                                                      Edwards SJ,
ÆBH, Webb EA,
cervical
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/product=
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115..1218
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/note= "hexaHis
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                                                                                                                                                                                                                                                                                                                                                                                                            note= "HPV-6
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 cancer
                                                                                                                                                                                                      Frazer I,
Williams
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       E4 "
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             E2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          used
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             used for
leader s
                                                                                                                                                                                                       MP;
                                                                                                                                                                                                                Margetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         condylomata acuminata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sequence
                                                                                                                                                                                                                  MB,
                                                                                                                                                                                                                  McMillan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          purification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              form
                                                          human papillomavirus It was obtd. by
                                                                                                                                 constructs
cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             pTrcHisA"
                                                                                                                                                                                                                  NAJ;
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Sequence 4770

BP;

1597 A; 890

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1071 G;

1212

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other;

Similarity 20; Conser

100.0%; llarity 100.0%; Conservative C

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Score 20; DB 1: Pred. No. 0.55; Mismatches

18; Ŧ,

Length 4770;

0;

Indels

0;

Gaps

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TGCTAATTCGGTGCTACCTG

20

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        A DNA molecule (AAT13413) codes for human papillomavirus 6a (HPV6a), the predominant HPV subtype found in biopsies of condyloma acuminata (benign lesions of the respiratory and genital mucosa). It was isolated from DNA extracted from a vulva condyloma acuminatum lesion
                                                                                                 WPI;
                                                                       DNA encoding human papillomavirus 6a vaccines against human papillomavirus
                                               Claim 1; Fig 1A-G; 46pp;
                                                                                                                Hofmann
                                                                                                                               (MERI ) MERCK
                                                                                                                                               22-SEP-1994;
                                                                                                                                                               18-SEP-1995;
                                                                                                                                                                                28-MAR-1996
                                                                                                                                                                                              WO9609375-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                     Human papillomavirus type 6a.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human papillomavirus type 6a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12-JUN-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAT13413 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2357
                                                                                                                ζ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TGCTAATTCGGTGCTACCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                             immunotherapy; genetic
                                                                                                                Jansen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                               & CO INC
                                                                                                                                               94US-0310468
                                                                                                                                                               95WO-US11859
                                                                                                                                                                                                                                     /*tag= g
/label= ORF-L2
5679..7292
                                                                                                                                                                                                                                                               4379..5803
                                                                                                                                                                                                             /product= major capsid protein
                                                                                                                                                                                                                      /label= ORF-L1
                                                                                                                                                                                                                                                                               /*tag=
                                                                                                                                                                                                                                                                                                                                       695..3830
                                                                                                                                                                                                                                                                                                                                                                                                                     ocation/Qualifiers
                                                                                                                                                                                                                                                                                       888..4163
                                                                                                                                                                                                                                                                                                               240..3585
                                                                                                                                                                                                                                                                      label ORF-E5
                                                                                                                                                                                                                                                                                                                                                                                             tag- a
label- ORF-E6
                                                                                                                                                                                                                                                                                                                                                              label- ORF-E7
16..2782
                                                                                                                                                                                                                                                                                                                        .abel= ORF-E2
                                                                                                                                                                                                                                                                                                                                               label- ORF-E1
                                                                                                                                                                                                                                                                                               abel- ORF-E4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CDNA;
                                                                                                                 즙
                                                                                                                                                                                                                                                                                                                                                                                       . 827
                                                                       papillomavirus
                                                                                                                                                                                                                                                                                                                                                                               6
                                                                                                                                                                                                                                                                                                                                                        റ
                                                English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8010
probe
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2376
                                                                                                                                                                                                                                                                                                                                                                                                                                                             immunisation; condyloma acuminata;
(see AAT13414) complementary to
                                                                       6a disease, e.g. condyloma

    used to treat and in

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                                                   The invention relates to a method for detecting the presence of a human CC papillomavirus (HPV) subtype in a nucleic acid containing sample. The CC method comprises amplifying the nucleic acid in the presence of a CC polymerase and a plurality of oligonucleotide sets, allowing digestion of CC each fluorescent probe during amplification to dissociate the fluorophore from the quencher molecule, detecting a change of fluorescence upon CC dissociation, and determining if the sample is positive for the HPV CC subtype if a change of fluorescence is detected in at least two emission CC maxima. Each oligonucleotide set mentioned above consists of a forward CC discriminatory PCR primer hybridising to a first location of an HPV CC subtype, a reverse discriminatory PCR primer hybridising to a second CC clocation of the HPV subtype downstream of the first location, and a CC fluorescent probe labelled with a quencher molecule and a fluorophore which emits energy at a unique emission maxima, the probe hybridising to CC a location of the HPV subtype between the first and the second locations, where each oligonucleotide set specifically hybridises to a different HPV capple of the present invention is useful in PCR-based assays for detecting HPV subtypes in clinical samples. This sequence represents a PCR primer used contained the function of the tecting HPV capped and the contained contained to the course of nucleic acid amplification. The method counters of the course of the c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 10
ABX12328/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local S
Matches 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Detecting the presence of a human papillomavirus subtype, using multiple fluorophores, in a nucleic acid-containing sample, useful PCR-based assays for identifying HPV subtypes -
                                         5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 15; Page
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2003-312914/30.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABX12328 standard; DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   end of the HPV subtype 6b L1 gene. The DNA can be used to develop vaccines against HPV6a, to treat conditions caused by HPV6a, for HPV serotyping, and to produce recombinant HPV6a polypeptides.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (MERI ) MERCK & CO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     23-AUG-2001; 2001US-314383P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            19-AUG-2002; 2002WO-US26964
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     06-MAR-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human papillomavirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Fluorescent multiplex HPV PCR assay primer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10-MAY-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABX12328;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ss;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   papillomavirus;
ss; polymerase;
                                       fluorescent multiplex
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZO,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8010
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              39;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            59pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       fluorophore;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HPV;
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                                         HPV PCR
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Pred. No. 0.58;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Dicello
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1715
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                                     assay of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                <u>ن</u>
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RESULT 11

RABS2985

ID AAS29

XX AAS29

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XX CAS29

XX Lung

KW Chick

Chick

FR 11-Jung

R 20-Jung

PR 11-Jung

PR 11-Ju
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Best Local S
Matches 18
                                                                                                                                                                                                                                                                                                                                                                              19-MAY-2000;
07-JUN-2000;
28-JUN-2000;
30-JUN-2000;
07-JUL-2000;
07-JUL-2000;
11-JUL-2000;
11-JUL-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      04-FEB-2000;
24-FEB-2000;
02-MAR-2000;
16-MAR-2000;
17-MAR-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Lung antigen protein; human; mouse; rabbit; goat; horse; cat; dog; chicken; sheep; humunosuppressive; antiarthritic; vasotropic; antirheumatuc; antiprolliferative; cytostatic; cardiant; neuroprotective; cerebroprotective; nootropic; antibacterial; virucide; fungicide; cancer; ophthalmological; vulnerary; gene therapy; autoimmune disease; neoplasm; hyperprolliferative disorder; breast; liver; cardiovascular disorder; ds; cerebrovascular disorder; nervous system disorder; bacterial infection; fungal infection; viral infection, ocular disorder; endocrine disorder; gastrointestinal disorder; renal disorder; respiratory disorder; gastrointestinal disorder; renal disorder; respiratory disorder; wound healing; skin aging; organ transplantation; food preservative; tissue regeneration; anti-infertility; food additive.
                                                                                                                                                                                                                                                                              14-JUL-
26-JUL-
26-JUL-
14-AUG-
14-AUG-
                                                                                                                                                                                                             14 - AUG-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
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    -2000;
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18; Conserv
                                                                                                                                                                                                                                                                              -2000
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2000US-0214886
2000US-0215135
2000US-0216847
2000US-0216880
2000US-0217487
2000US-0218290
2000US-022953
2000US-0224518
2000US-0224518
2000US-0225213
2000US-0225213
2000US-0225216
2000US-0225216
2000US-0225276
2000US-0225276
2000US-0225275
2000US-0225275
2000US-0225275
2000US-0225275
2000US-0225275
2000US-0225758
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3-0190076
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3-0184664
3-0186350
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          #55.
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    02-OCT 2000
02-OCT 2000
13-OCT 2000
13-OCT 2000
20-OCT 2000
20-OCT
  -NOV-2000;
-NOV-2000;
-NOV-2000;
-NOV-2000;
-NOV-2000;
-NOV-2000;
-NOV-2000;
-NOV-2000;
2000US-0246478.
2000US-0246523.
2000US-0246525.
2000US-0246526.
2000US-0246526.
2000US-0246528.
2000US-0246532.
2000US-0246610.
2000US-0246611.
2000US-0246613.
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2000US-0246613.
2000US-0246613.
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2000US-0241808.
2000US-0241809.
2000US-0241826.
2000US-0244617.
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2000US-0239935.
2000US-0239937.
2000US-0240960.
2000US-0241221.
2000US-0241785.
2000US-0241786.
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2000US-023365

2000US-0234223

2000US-0234274

2000US-0234997

2000US-0234998

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2000US-0235836
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2000US-0246475.
2000US-0246476.
2000US-0246477.
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novel

human

respiratory antigen

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Sequences AAS2991-AAS30164 represent genomic DNA molecules, which encode CC the lung antigen polypeptides of the invention. Lung antigen polypeptides CC and their associated polynucleotides are useful in the diagnosis, CC treatment and prevention of various types of disorders in e.g. humans, CC mice, rabbits, goats, horses, cats, dogs, chickens or sheep. A CC pathological condition can be determined by detecting the presence or a mutation in a lung antigen polynucleotide. The treatable CC disorders include autoimmune diseases such as rheumatoid arthritis, CC hyperproliferative disorders such as nervous system disorders such as cerebral ischaemia, nervous system disorders such as CC cardiovascular disorders such as cerebral infection, endocrine disorders such as CC conh's disease, infections caused by bacteria, viruses and fungi, CC coular disorders such as corneal infection, endocrine disorders such as CC crohn's disease, renal disorders such as glomerulonephritis and CC crohn's disease, renal disorders such as glomerulonephritis and CC crohn's disease, renal disorders such as glomerulonephritis and CC consistency disorders such as asthma and pleurisy. The polypeptides can also be used to aid wound healing, to prevent skin aging due to sunburn, CC to maintain organs before transplantation, to regenerate tissues and in CC chemotaxis. The polypeptides can also be used as a food additive or CC preservative to increase or decrease storage capabilities.

CC Note: The sequence data for this patent did not form part of the printed CC specification, but was obtained in electronic format directly from WIPO or at fire vino intrombrable and retrease.
                                                                              Query Match
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Pred. No. 80;
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    RESULT 12
AAS28494
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22-AUG-2000

23-AUG-2000

23-AUG-2000

30-AUG-2000

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01-SEP-2000
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17-MAR-2000;
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26-JUL-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    n; respiratory antigen; respiratory disorder; throat disorder; disorder; nose disorder; lung cancer; gene therapy; cytostatic; allergic; anti asthmatic; anti inflammatory; olfactory; iratory active; ds.
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                  2000US-0229345.
2000US-0229509.
2000US-0229513.
2000US-0230437.
2000US-0230438.
2000US-0231242.
2000US-0231243.
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2000US-0227182.
2000US-0227709.
2000US-0228924.
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2000US-0186350.
2000US-0189874.
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2000US-0198123.
2000US-0205515.
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2000US-0225270.
2000US-0225447.
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2000US-0225266.
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2000US-0226279.
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HPI; Rosen

also

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Matches

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14-SEP-2000; 14-SEP-2000; 14-SEP-2000; 21-SEP-2000;

21-SEP-2000; 25-SEP-2000; 25-SEP-2000;

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RESULT 13
AAS29864
ID AAS29
XX AS29
XX AS29
XX 21-NC
DT 21-NC
DT 21-NC
XX Lung
KW Lung
KW Chick
KW antir
KW antir
KW ophth
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AAS28161-AAS28764 represent genomic sequences encoding for novel human respiratory antigens.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at the vice in the ball that the ball the control of the printed specification.
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17-NOV-2000;
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05-DEC-2000;
06-DEC-2000;
06-DEC-2000;
06-DEC-2000;
08-DEC-2000;
          Lung antigen protein; human; mouse; rabbit; goat; horse; cat; dog; chicken; sheep; lumunosuppressive; antiarthritic; vasotropic; antirheumatic; antiproliferative; cytostatic; cardiant; neuroprotective; cerebroprotective; nootropic; antibacterial; virucide; fungicide; cancer; ophthalmological; vulnerary; gene therapy; autoimmune disease; neoplasm; hyperproliferative disorder; breast; liver; cardiovascular disorder; ss; hyperproliferative disorder; breast; liver; cardiovascular disorder; ss;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI;
                                                                                                                              Human
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RESULT 14
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CC Note: The sequence data for this patent did not form part of the printed cc specification, but was obtained in electronic format directly from WIPO
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11-DEC-2000;
05-JAN-2001;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1;
                                                                                                                                                                            Human; respiratory antigen; respiratory disorder; throat disorder; lung disorder; nose disorder; lung cancer; gene therapy; cytostatic; anti allergic; anti asthmatic; anti inflammatory; olfactory;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequences AAS29839-AAS29930 represent cDNA molecules, which encode the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (HUMA-) HUMAN GENOME SCI INC
31-JAN-2000; 2000US-0179065
                                17-JAN-2001; 2001WO-US01333
                                                                                               WO200155448-A1
                                                                                                                                                                                                                                             Novel cDNA encoding
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                                                                                                                                                                                                                                                                                                                 AAS28028;
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                                                                                                                                sapiens.
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DB; AAU18577.
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17; Conser
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; 2000US-0254097.
; 2001US-0259678.
                                                                                                                                                                                                                                                                                                                                                cDNA; 287
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89.5%;
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19-MAY-2000;
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14-SEP-2000

14-SEP-2000

21-SEP-2000

21-SEP-2000

25-SEP-2000

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27-SEP-2000

27-SEP-2000

29-SEP-2000

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21-AUG-2000
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    Isolated polypeptide disorders related to cancers and also for
                                                               2001-476224/51.
DB; AAU17844.
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RESULT 15
ABZ52394/c
ID ABZ52394 standard; cDNA; 907
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                                                                                                         Detection of expression the fermentation and gro
                                                                                                                                                                           Machida
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(NARE-)
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                                                                                                                                                                                                                                                                   22-MAR-2002; 2002WO-IB00890.
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                                                                                                                                                                                                                                                                                                                                                                     fermentation;
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89.5%;
                                                                                                          growth conditions of the fungus,
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The invention relates to a polynucleotide having any of 6006 specific sequences (ABZ50888-ABZ56893), which are expressed by a fungus under specific culture conditions including one or more of eutrophic, oligotrophic, solid, early germination, alkaline, high temperature, low temperature or maltose culture or polynucleotides stringently hybridising to these sequences. The polynucleotides are useful for monitoring the

Claim 1;

SEQ

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NO 1507; 48pp +

Sequence Listing;

Japanese

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CC progress of fermentation and the growth conditions of a fungus, CC especially of Aspergillus oryzae which is widely used in industrial CC fermentation. Also monitoring for fungal contamination.

CC Note: The sequence data for this patent did not form part of the printed Specification, but was obtained in electronic format directly from WIPO CC at ftp.wipo.int/pub/published_pct_sequences.

XX Sq Sequence 907 BP; 249 A; 208 C; 205 G; 243 T; 2 other;

Query Match 79.0%; Score 15.8; DB 25; Length 907;

Best Local Similarity 89.5%; Pred. No. 91;

Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 TGCTAATTCGGTGCTACCT 19

Db 154 TGCTTCTTCGGTGCTACCT 136

Search completed: August 23, 2003, 10:38:19

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GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.
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Title:
Perfect score:
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## SUMMARIES

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	AX301234 LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM REFERENCE AUTHORS TITLE JOURNAL	110 110 110 110 110 110 110 110 110 110	0000	Result No.
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RESULT 3
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                                                                                                                                                                                                                                                                                                                                                                    source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N EU52,, GI:41, S E05257.1 GI:41, S JP 1993192200-A/27.

S JP 1993192200-A/27.

Synthetic construct artificial sequences.

I (bases 1 to 20)
HORS Okazawa, K., Shimada, M., Katou, I., Fukushima, M. and Fujinaga, K.

DETECTION OF HUMAN PAPILLOMA VIRUS
Patent: JP 1993192200-A 27 03-AUG-1993;
                                                                                                                                                                                                                                                 Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   source
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TAKARA SHUZO CO LTD
OS Artificial gene
OC Artificial seque
PN 1993192200-A/
PD 03-AUG-1991 JP 1
PR 20-AUG-1990 JP 9
PI OKAZAWA KAZUHIDE
FUXUSHIWA MICHIO,
PI FUJINAGA KEI
PC C1201/70,01201/6
CC Strandedness: Si
CC typothetical: NO.
CC anti-sense: NO.
                                     synthetic construct
                                                  E05247.1 GI:2173437
JP 1993192200-A/17.
                                                                                   Part of DNA sequence E05247
                                                                                                             E05247
                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Primer for amplifying Human papillomavirus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Artificial gene
Artificial sequence; Genes.
JP 193192200-A/27
03-AUG-1993
19-AUG-1991 JP 1991230839
20-AUG-1990 JP 90P 217067
OKAZAWA KAZUHIDE, SHIMADA MAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TGTCAAAAACCGTTGTGTCC 20
                                                                                                                                                                                                                                   100.0%;
llarity 100.0%;
Conservative (
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C12Q1/70,C12Q1/68;
strandedness: Single;
                                                                                                                                                                                                                                                                                                                                                                                                      hypothetical: No;
                                                                                                                                                                                                                                                                                                                                                                                                                   topology: Linear;
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ilarity 100.0%;
Conservative (
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                                                                                                                                                                                                                                                                                                /organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
5 c 4 g 6 t
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/mol_type="genomic DNA"
/db_xref="taxon.32630"
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Pred. No. 4.8
0; Mismatches
                                                                                      Human
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Pred. No. 4.8
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4.8;
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                                                                                   linear
us 31.
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                                                                                              PAT 29-SEP-1997
                                                                                                                                                                                                                            0;
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AUTHORS
TITLE
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AUTHORS
JOURNAL
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ACCESSION
VERSION
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SOURCE
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PPHE67
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AUTHORS
TITLE
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Best Local :
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OC Artificial gene
OC Artificial sequence; Genes.
OS Human papillomavirus
PN JP 1993192200-A/17
PD 03-AUG-1993
PF 19-AUG-1993 JP 1991230839
PR 20-AUG-1990 JP 90P 217067
PI OKAZAWA KAZUHIDE, SHIMADA MASJ
FUKUSHIMA MICHIO,
PI FUJINNGA KEI
PC C1201/70,C12Q1/68;
CC strandedness: Single;
CC topology: Linear;
CC hypothetical: No;
CC anti-sense: No.
                                                                                                                                                                                       Submitted (26-FEB-1992) Kei Fujinaga, Cancer Research Institute, Sapporo Medical College, Department of Molecular Biology; S1, W17, Chuo-ku, Sapporo 060, Japan (Tel:011-611-2111, Fax:011-615-3099)
                                                                                                                                                                                                                                                       2 (bases 1 to 803)
Fujinaga, K.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                 Human papillomavirus
Human papillomavirus
Viruses; dsDNA viruses,
                                                                                                                                                                                                                                                                                                 Fujinaga, K.
Unpublished
                                                                                                                                                                                                                                                                                                                       Papillomavirus.
1 (bases 1 to 803)
                                                                                                                                                                                                                                                                                                                                                                                                         Human papillomavirus gene
D10597 D01089
D10597.1 GI:535788
                                                                                                                                                                                                                                                                                                                                                                                                 E6 protein;
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|||||||| |||||||||||
TGTCAAAGACCGTTGTGTCC 20
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1 (bases 1 to 20)

Okazawa,K., Shimada,M., Katou,I., Fukushima,M. and Fujinaga,K.

DETECTION OF HUMAN PAPILLOMA VIRUS

Patent: JP 1993192200-A 17 03-AUG-1993;

TAKARA SHUZO CO LTD

OS ARTIGUS.
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/product="E6 protein"
/protein_id="BAA01447.1"
/protein_id="BAA01447.1"
/db_xref="GI:535789"
/translation="MFQDPAERPYKLHDLCNEVEESIHEIGLNCVYCKQELQRSEVYD
/translation="MFQDPAERPYKLHDLCNEVEESIHEIGLNCVYCKQELQRSEVYD
FACYDLCIVYREGQPYGVCMKCLKFYSKISEYRRYRYSVYGETLEKCCNKQLCHLLIR
CITCQKPLCPVEKQRHLEEKKRFHNIGGRWTGRCMSCWKPTRRETEV"
                                                                                                                      Organism="Human papillomavirus"
/mol_type="genomic DNA"
/isolate="Type Sapporo-A"
/db_xref="taxon:10566"
                                                                                              codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
5 c 5 g 6 t
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                                                                                                                                                                                                                                                                                                                                                                                         E7 protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 18.4;
Pred. No. 38;
                                                                                                                                                                                                                                                                                                                                                  no
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
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VERSION
KEYWORDS
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PPH35CG
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MEDLINE
PUBMED
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MEDLINE
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AUTHORS
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                                      gene
    CDS
                                                                                                                                                                                                                                  CAAT_signal protein_bind
                                                                                                                                                                                                                                                                                           protein_bind
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                                                                              TATA_signal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 (bases 1 to 7851)
Marich, J.E., Pontsle
Dubensky, T.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          complete genome; major capsid protein; minor capsid protein; regulatory protein; replication protein; transformer protein Human papillomavirus type 35

Human papillomavirus type 35
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Original source text: Human papillomavirus type carcinoma DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   human papillomavirus type
Virology 186 (2), 770-776
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The phylogenetic relationship and complete nucleotide sequence human papillomavirus type 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Virology 159, 187-190 (1991)
87265470
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cervix
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Lorincz,A.T., Quinn,A.P., Lancaster,W.D. and Temple,G.F.
A New Type of Papillomavirus Associated with Cancer of the Uterine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Papillomavirus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /translation="MHGEITTLQDYVLDLEPEATDLYCYEQLCDSSEEEEEDTIDGPAG
QAKPDTSNYNIVTSCCKCEATLRLCVQSTHIDIRKLEDLLMGTFGIVCPGCSQRA"
1 127 c 190 g 204 t
  /gene="E6"
110. .559
                                                                              /function="gene transcription"
54. .59
                                                                                                                                                                                                                                                     complement(18. .26)
                                      /note-"putative"
                                                                                                                                                                                                                                                                         /bound_moiety="Sp-1"
                                                                                                                                                                                                                                                                                                                   /standard_name="LCR"
                                                                                                                                                                                                                                                                                                                                                    /mol_type="genomic DNA"
//solation_source="cervical carcinoma"
//db_xref="taxon:10587"
/oin(7092. .7851,1. .109)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /product="E7 protein"
/protein_id="BAA01448.1"
/db_xref="GI:535790"
                                                                                                                                                                                              /bound_moiety="E2"
                                                                                                                                                                                                              note-"putative"
                                                                                                                 bound_moiety-"E2"
                                                                                                                                   note-"putative"
                                                                                                                                                                          function="gene transcription"
                                                                                                                                                                                                                                                                                                                                                                                                                                             organism-"Human papillomavirus
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                                                                                                                                                                                                                                                                                                           runction="regulatory region"
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95.0%;
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Pred. No. 41;
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pe 35
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 type
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                                                                                                                   CDS
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GIYRPIFKKCTRWKSYISFRCKALSIVHIMPTFTYYININAGKDDRWPYLHSRVVVFT
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405. .416
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /translation="MFQDPAERPYKLHDLCNEVEESIHEICLNCVYCKQELQRSEVYDFACYDLCIVYREGOPYGVCMKCLKFYSKISEYRWYRYSVYGETLEKQCNKQLCHLLIRCTCCKPLCPVEKQRHLEEKKRFHNIGGRWTGRCMSCWKPTRRETEV"
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RPTTRLGLYSKGTQQVKVVDPAFMTSPAKLITYDNPAYEGLNPDTTLQFEHEDISLAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DDDEMDI IALHRPALTSRKGTIRYSRVGNKRTMHTRSGKAIGARVHYYQDLSSITEDI
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7695. .7700
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7671. .7676
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TITLE
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JOURNAL
MEDLINE
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1 Similarity 95.0%;
19; Conservation
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25 TGTCAAAAACCGCTGTGTCC 444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human papillomavirus type 35H
Human papillomavirus type 35H
Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Delius.H.
Direct Submission
Direct Submission
Submitted (06-AUG-1993) H. Delius, Deutsches
Submitted (06-AUG-1993) H. Delius, Deutsches
Krebsforschungszentrum, Abteilung ATV, Im Neuenheimer Feld 506,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              El gene; E2 gene; E4 gene; I gene; L2 gene; Late protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Primer-directed sequencing of human Curr. Top. Microbiol. Immunol. 186,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Delius, H. and Hofmann, B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Papillomavirus.
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CITCQKPLCPVEKQRHLEEKKRFHNIGGRWTGRCMSCWKPTRRETEV"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            clone="insert in BamHI site of pBR322"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 18.4;
Pred. No. 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7879 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  35H genomic DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2387
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    papillomavirus types
13-31 (1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      E7 gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        early protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7851;
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RESULT 7
PPH31A
                                                                                                                                                                                                                                                                                                                                     BASE COUNT
ORIGIN
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Best Local :
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                                                                                                              425 TGTCAAAAACCGCTGTGTCC 444
                                                                                                                                           1 TGTCAAAAACCGTTGTGTCC
                                                                                                                                                                                                                            19;
                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                     2570
                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                 /gene="L1"
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/db_xref="SSISS-PROT: P27232"
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/translation="MSLWRSKBATVYLPPVSVSKVVSTDEYVTRTNIYYHAGSSRLLA
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GYEVGRGQPLGVGISGHPLLNKLDDTENSKKYGNSCDENDTTCAANK
CRPPTGEHWGKGTPCNANQVKAGECPELELNTVLQDGDMVDTGFGAMDFTTLQANKS
DVPLDICSSICKYPDYLKMVSEPYGDMLFFYLRREQMFVHLFNRAGTVGETVPADLY
IKGTTGTLPSTSYFPTPSGSMVTSDAQIFNKFYWLQRAQGHNNGJCWSNOLFVTVVDT
FRSTNNSVCSAVSSSDSTYKNDNFKEYLRHGEEYDLQFIFQLCKITLTADVMTYTHSM
NPSILEDWNFGLTPPPSGTLEDTYRYVTSQAVTCQKPSAFKFKDDPLKNVTFWEVDLK
NPSILEDWNFGLTPPPSGTLEDTYRYVTSQAVTCQKPSAFKFKDDPLKNVTFWEVDLK
SEKFSADLDQFPLGRKFLQAGLKARPWFRLGKRAAPASTSKKSSTKRRKVKS"
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2714.
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/translation="MRHRSTKRVKRASATQLYRTCKAAGTCPPDVIPKVEGNTVADQ
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GPLDSSIVSLVEETSFIESGAPVVTPRVPPTTGFTITTSTDTTPAILDVTSISTHDNP
TETDPSVLHPPTPAETSGHFVLSSSSISTHNYEEIPMDTFIVSTDSNNITNSTPIPSC
RPTTRIGLYSKCTQQVKVVDPAMTSPAKLITVDNPAYEGLNPDTTLOFEHDDISLAF
PDPEMDIIALHRPALTSRKGTIRVSRVGNKTIMHTRSGKAIGARVHYYQDLSSITEDI
ELQPLQHVPSSLDHTTVSTSLNDGMFDIYAPIDTEDIIFSASSNVTLYTTSNYAYVP
SNTTIPLSSGYDIPTAACPDIVENSNTITNTVLPVPTGPIYSIIADGGDFYLHPSYYL
KRRRKRIPYFFADVSVAV"
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/gene="E2"
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NNNISPRLKAICIENKNTAAKRRLFELPDSGYGNSEVEIQQIQQVEGHDTVEQCSMGS
GDSITSSSDERHDETPTRDIQILKCSNANAMLAKFKEISTELLISTELLISEKSKST
CTDMCVAAFGIAPSVAESLKTLIKPYCLYIHAQCLSCSWGMVILALLREKCAKNRTTI
EKLLSKLLCISAASMLIQPPKLRSTPAALYWFKTAMSNISEVDGETPBWIQRQTVLQH
SFNDAIFDLSEMVQWAYDNDFIDDSDIAYKYAQLAETNSNACAFLKSNSQAKIYKDCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /gene="L1"
5601. .7109
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4211. .5
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HGVPKKNCILIYGAPNTGKSLEGMSLMHFLQGAIISYVNSKSHEWLQPLYDAKIAMLD
DATSPCWAYIDQYLRNALDGNPISLDVKHKALVQLKCPPLLITSNINAGKDDRWPYLH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /translation="M" 4211. .5620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /product="early protein"
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/db_xref="GI:584036"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /codon_start=1
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95.0%;
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Pred. No. 4
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                                                                                                                                                                                                                                                                        Length 7879;
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JOURNAL
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AUTHORS
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ACCESSION
VERSION
KEYWORDS
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ORGANISM
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TATA_signal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Original source text: Human papillomavirus type 31 DNA. Draft entry and computer-readable copy of sequence [1] kindly submitted by M.D.Goldsborough, 05-JUL-1989.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Goldsborough, M.D., Disilvestre, D., Temple, G.F. and Lorincz, A.T. Nucleotide sequence of human papillomavirus type 31: a cervical neoplasia associated virus Virology 171 (1), 306-311 (1989) 89299478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human papillomavirus type 31
Human papillomavirus type 31
Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       complete genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             J04353.1
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1 (bases 1 to 7912)
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THSERENETPTRNILQVLKTSNGKAAMLGKFKELIGVSFMELIRPFQSNKSTGTDMCV
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LCISTNCMLIQPPKLRSTAAALYWYRTGMSNISDVYGETPENIERGTVLQHSENDTT
                                                                                                                                                                                                                                                                                                                                            /gene="E1"
862. .2751
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560. .856
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/standard_name="Splice donor"
403. .414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /translation="MFKNPAERPRKLHELSSALEIPYDELRLNCVYCKGQLTETEVLD
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CITCQRPLCPEEKQRHLDKKKRFHNIGGRWTGRCIACWRRPRTETQV"
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862. .2751
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/db_xref="GI:459916"
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                                                                                                                                                                                                                                                                                            /note="ORF E1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                560. .856
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /standard_name="Splice acceptor"
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                                                                                                                                                                                                                                                                                                                    'gene="El"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /gene="E7"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /gene="E4"
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PSIVSLVEESGIVDVGAPAPIPHPTTSGFDIATTAOTTPAILDVTSVSTHEHPTFTD
PSVLQPPTPAETSGHLLISSSSISTHNYEEIPMDTFIVSTNNENITSSTPIPGVRRPA
RLGLYSKATQQYKVIDPTFLSAPKQLITYENPAYETVNAEESLYFSNTSHNIAPDPDF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /gene="L2"
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3816. .4070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3816.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KAREMGIHSINHQVVPALSVSKAKALQAIELQMMLETLNNTEYKNEDWTMQQTSLELY
LTAPTGCLKKHGYTVEVQFDGDVHNTMHYTNWKFIYLCIDGQCTVVEGQVNCKGIYYV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WHYIDNYLRNALDGNPVSIDVKHKALMQLKCPPLLITSNINAGKDDRWPYLHSRLVVF
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                                                                                                                       note="ORF L1 from bp 5516 to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         codon_start=1
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AUTHORS
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AE013763
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JOURNAL
PUBMED
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423 TGTCAAAGACCGTTGTGTCC 442
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12142430
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                                                                                                                                                                                                                                                                                                                                                                                                                                        l (bases 1 to 10909)
Deng,W., Burland,V., Plunkett,G. III, Boutin,A.,
Liss,P., Perna,M.T., Rose,D.J., Mau,B., Zhou,S.,
Fetherston,J.D., Lindler,L.E., Brubaker,R.R., Pla
Straley,S.C., McDonough,K.A., Nilles,M.L., Matson
Blattner,F.R. and Perry,R.D.
Genome Sequence of Yersinia pestis KIM
J. Bacteriol. 184 (16), 4601-4611 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         l Similarity
19; Conser
                                                                                                                                                                         Submitted (21-FEB-2002) Genetics, University Henry Mall, Madison, WI 53706, USA Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Yersinia pestis KIM
Yersinia pestis KIM
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Yersinia pestis KIM section AE013763 AE009952 AE013763.1 GI:21958388 ...
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /standard_name="keratinocyte-dependant enhancer" 7868. .7879
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HSMNPAILEDWNFGLTTPPSGSLEDTYRFVTSQAITCQKTAPQKPKEDPFKDYVFWEV
NLKEKFSADLDQFPLGRKFLLQAGYRARPKFKAGKRSAPSASTTTPAKRKKTKK"
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GCKPPIGEHWGKGSPCSNNAITPGDCPPLELKNSVIQDGDMVDTGFGAMDFTALQDTK
SNVPLDICNSICKYPDYLKMVAEPYGDTLFFYLRREQMFVRHFFNRŞGTVGESVPTDL
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116. .1126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /standard_name="glucocorticoid responsive element"
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7406. .7420
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1364 c 1572 g 2448 t
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                                                                                                                                                          .10909
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95.0%;
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                                                                                                                                                                                                                              of Wisconsin,
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'note="synonym: y1598'

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gene
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/function="putative"
/function="putative"
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residues 1 to 337 of 337 from E. coli K12 : B2319;
residues 1 to 337 of 337 from GenPept : >gh AAL21270.1|
(AE008806) putative aspartate-semialdehyde dehydrogenase
[Salmonella typhimurium LT2]"
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ASAHGKAAVDDLAGQSAKLLNGIPAEPGAFFVAGEARAFLADEEGSVSEERRLVDQ
VRKVLQDEGLIFTVSCLQSSAVLDGIPAEPGAFFVALAEREERRELENCDDIOLSEED
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2901. 3971
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2137. .2826
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to residues 1 to 216 of 219 from E. coli K12: B2317;
residues 1 to 225 of 229 are 85.18 pct identical to
residues 1 to 216 of 219 from GenPept : >gb|AAL/21268.1|
(AE008806) putative DedA family [Salmonella typhimurium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /trans__table=11
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MPLDAEKMERAAQCLLGENDFTSFRAVQCQSRTPWRNVKHVKVTRHGAYIVVDIKANA
FVHHYRNIVGSLIEIGCGNQDVTWMAELLALKDRTRAAATAKADGLYLVSVDYPDHF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="residues 20 to 290 of 293 are 78.22 pct identical to residues 4 to 270 of 270 from E. coli K12: B2318; residues 20 to 290 of 293 are 78.59 pct identical to residues 4 to 270 of 270 from GenPept: >emb|CAD07600.1| (AL627274) tRNA pseudouridine synthase A [Salmonella enterica subsp. enterica serovar Typhi]"
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modification"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /gene="truA"
/note="synonym: y1599"
1126. .2007
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LY"
1126. 2007
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2137. .2826
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                                                                                                                                           /gene="accD"
                                 gene
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FKQAKLDVVILEVGLGGRLDAFNIVDSDVAATTSIALDFTDWLGYDRESIGREKAGVF
RGGKPAVVGEPDMPQSIADVAAFLGAGLYRRDVAMKFSQGEPFDQQEPVDQGINGHW
QCGERQLTGLEVPNVPLANATALAVLHYSELFUSDEAIRQGLQAASLPGGFQVVSEQ
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GSALPELNALSGLNGQVKPYTTSR"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /gene-"dedD"
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residues 3 to 239 of 242 are 56.72 pct identical to
residues 3 to 239 of 242 are 56.72 pct identical to
residues 1 to 218 of 220 from GenPept:
>pb|AAG57443.1|AE005463_6 (AE005463) putative lipoprotein
[Escherichia coli 0157:H7 EDL933]"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       folylpolyglutamate synthase; dihydrofolate synthase, also has formylTHF polyglutamate synthase activity [Salmonella typhimurium LT2]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note-"dihydrofolate synthetase; residues 31 to 458 of 460 are 65.42 pct identical to residues 5 to 414 of 422 from E. coli KI2 : B2315; residues 27 to 458 of 460 are 65.20 pct identical to residues 1 to 414 of 422 from Genept : 250 [AAL21266.1] (AE008806) multifunctional
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="synonym: y1602"
4142. 5524
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             biosynthesis"
//note-"residues 53 to 350 of 356 are 86.24 pct identical //note-"residues 1 to 296 of 304 from E. col1 Kl2 : B2316; to residues 1 to 296 of 356 are 86.91 pct identical to residues 53 to 350 of 356 are 86.91 pct identical to residues 1 to 296 of 304 from GenPept : -ygb|AAL21267.1| (AE008806) acety|COA carboxylase, beta subunit [Salmonella typhlmurium LT2]"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="synonym: y1603"
5638. .6366
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/gene="dedD"
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component, beta subunit"
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/codon_start=1
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SOURCE
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Best Local S
Matches 18
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                                                                                                                                                                                                                                                              Submitted (03-JUL-2001) Takuji Sasaki, National Institute of Agrobiological Sciences, Rice Genome Research Program; Kannondai 2-1-2, Tsukuba, Ibaraki 305-8602, Japan (E-mail:tsasaki@nlas.affrc.go.jp, URL:http://rgp.dna.affrc.go.jp/, Tel:81-298-38-7441, Fax:81-298-38-7468)
On Oct 26, 2002 this sequence version replaced gi:22775423.
Genes were predicted from the integrated results of the following: GENSCAN (http://CCR-081.mit.edu/GENSCAN,html), FGENESH (http://www.softberry.com/), GeneMark.hmm (http://www.softberry.com/), GeneMark.hmm (http://www.tigr.org/tdb/glimmerm/glmr.form.html), RiceHMM (http://rgp.dna.affrc.go.jp/RiceHMM/), SplicePredictor (http://foinformatics.lastate.edu/cgi-lin/sp.cgi), BLASTN and BLASTX. The genomic sequence was searched against NCBI NonRedundant
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ب
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sasaki,T., Matsumoto,T. and Yamamoto,K. Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Oryza sativa (japonica cultivar-group) genomic DNA, chromosome
A gene with identity or significant homology to a protein is classified based on the protein name to indicate the homology level such as same name, 'putative-' and '-like protein'. A gene without significant homology to any protein but with EST homology (covering
                                                                                                   (ftp://ncbi.nlm.nih.gov/blast/db) and the cDNA sequence database at RGP. Protein homologies of the coding regions were searched against NCBI NonRedundant Protein database with BLASTP. ESTs represent the identified cDNA sequences using BLASTN with the corresponding DDBJ accession no. and RGP clone ID.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Published Only in Database (2001)
2 (bases 1 to 102178)
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/function="membrane; colicin V production; residues 1 to
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160 of 169 are 83.12 pct identical to residues 1 to 160 of 169 are
83.12 pct identical to residues 1 to 160 of 162 from
Genrept: 'spb|ARL21264.1| (AE008806) membrane protein
required for colicin V production [Salmonella typhimurium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /product-"membrane protein"
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6663. .7172
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94.7%;
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Pred. No. 1
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     CDS
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'unknown' protein. A gene predicted by two or more gene prediction programs is classified as a 'hypothetical' protein according to IRGSP standard. A gene predicted by a single gene prediction program is also classified as a probable 'hypothetical' protein and is included as a miscellaneous feature of the sequence. The orientation of the sequence is from -21M13 to M13rev of the BAC clone. This sequence of OJ1060_D03 clone has an overlap with OJ1117_E01 clone(DDBJ: AP003747)at 5' end and an overlap with OJ1113_E01(DDBJ: AP005437) at 3' end. The nucleotide sequence of this BAC clone was generated by combining Monsanto and RGP-Japan sequencing data. Detailed information on overlap and assembly quality together with annotation of this entry is available at http://rgp.dna.affrc.go.jp/GenomeSeq.html.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                almost the entire length of partial sequence) is classified as an
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hypothetical ORF
predicted by GlimmerM"
complement(4270. .4578)
/gene="0J1060_D03.2"
complement(4270. .4578)
                                                                                                                                                                                                                                                                                                                                                                                                        JOHN (**--
11030. 11337)
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/oin(8621. _8754,8874. .8983,9860. .9930,10812. .10932,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /gene="0J1060_D03.1"
1311. .1511
                                                                                                                            /protein_id="BAC22263.1"
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YSPRTAFIEDFFSTDPPQEEYGMDYWHAAPQVTQPTQETEAGQGPDVTPQQTARDRHP
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VVGEDEMLHTISLTPPVIPLPSLSSSLSSLSLFFAGSACTDGLVGSGAAAGDLGEAAP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                complement(join(5870. .6466,6570. /gene="OJ1060_D03.3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                complement(join(5870. .6466,6570. /gene="OJ1060_D03.3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /protein_id="BAC22261.1"
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/note="hypothetical protein
predicted by GeneMark.hmm etc."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Oryza sativa
/mol_type="genomic DNA"
/cultivar="Nipponbare"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="hypothetical protein predicted by GeneMark.hmm etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /clone="0J1060_D03"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PSPPLATSRSRHAGMISFGYHSTTGKYKIVHFPSNGGLVDEVTLGGTASSSSPPAMAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /gene="0J1060_D03.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /db_xref="taxon:39947"
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/gene="071060_D03.4"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       join(8621.
12019. .12453
/gene="OJ1060_D03.5"
12019. .12453
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               codon_start-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /codon_start=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8754,8874. .8983,9860. .9930,10812. .10932,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       not included in IRGSP standard.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (japonica cultivar-group)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .6647))
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CDS
                                                                                                                                                                                                                                                                               gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            misc_feature
                                                                                                                                                                                                                                                                                                                      /gene-"0J1060_D03.10"
/note-"probably inactive due to frameshift(s)
probably inactive due to stop codon(s) in CDS
pseudogene, hydroxyproline-rich glycoprotein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /protein_1d="BAC22266.1"
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/db_xref="GI:24414016"
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ESTARYDGGVGAGP"
                                                                                                                                                                                                                                                                                                                                                                                                                                          /gene="0J1060_D03.10"
28336. .31791
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="hypothetical protein predicted by GENSCAN etc."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           complement(join(26731. .27006,27068. .27145))
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                                                                                                                                       /note="hypothetical protein
predicted by gm etc."
                                                                                                                                                                                                                            /gene="0J1060_D03.11"
36755. .37150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          complement(join(26731. .27006,27068. .27145))
/gene="OJ1060_D03.9"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             complement(join(19591. .19658,20059.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                complement(join(19591. .19658,20059.
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aaplervepfylacvralgpdaapdarrtaaarirllakhrsdireligvsgaipalv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                \tanslation="MRCAMIMHRLEDHARARVQSAHLLTVNUTVPSPLLAALPNURRCH
LPNGEKKTPPKRSRCLHVSTSHRAKAATPMPITPYYYSSGANARGRGPSRSGARAAA
AATWHIGEEOTNGKKCUSLLPQPPKVKPPGANCWMPAAHAMAP"

join(12948, 14258,15290. .15376,16109. .16198)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            pseudogene, Taml transposon protein TNP2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              predicted by GENSCAN"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="This category is hypothetical ORF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFAVVALLQLCSECPRNRALLVREGAIPPLVALSQSGSARAKHKAETLLGYLREQRQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GAVVPLIHLVGERGSGTSEKAMVVLASLAGIVEGRDAVVEAGGIPALVETIEDGPARE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LLSLSGIEENRATIGACGAIPPLVALLSAGSTRGKKDALTTLYRLCSARRNKERAVSA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PLLRSTDPVAQESAVTALLNLSLEERNRSAITAAGAIKPLVYALRTGTASAKQNAACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                predicted by GlimmerM etc."
                                                                                                                                                                                                /gene="0J1060_D03.11"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="deletion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /gene-"0J1060_D03.8"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /gene-"OJ1060_D03.8"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /protein_id="BAC22265.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="arm repeat containing protein homolog-like"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /gene="0J1060_D03.6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /protein_id="BAC22264.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="hypothetical protein
                                                                                                                   codon_start=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CRVEPVAASSLAFIVLRCVTFSLTPTSGSAAPSIWVTYSYT"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              _xref="GI:24414014"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                not included in IRGSP standard.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .20179))
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         . 20179))
                                                                                                                                                                                                                                                                                                                                                                                          in CDS
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SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 10
AC107604/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               밁
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Š
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VERSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EOCUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Allen, C., Allen, H., Alsbrooks, S., Amin, A., Angulano, D.,
Anyalebechi, V., Aoyagi, A., Ayodeji, M., Baca, E., Baden, H.,
Baldwin, D., Bandaranaike, D., Barber, M., Barnstead, M., Benahmed, F.,
Blswalo, K., Blair, J., Blankenburg, K., Blyth, P., Brown, M.,
Bryant, N., Buhay, C., Burch, P., Burrell, K., Calderon, E.,
Cardenas, V., Carter, K., Cavazos, I., Ceasar, H., Center, A.,
Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Y., Chen, Z., Chu, J.,
Claveland, C., Cockrell, R., Cox, C., Coyle, M., Cree, A., D'Souza, L.,
Davila, M.L., Davis, C., Davy-Carroll, L., De Anda, C., Dederich, D.,
Delgado, O., Denson, S., Deramo, C., Ding, Y., Dinh, H., Divya, K.,
Draper, H., Dugan-Rocha, S., Dunn, A., Durbin, K., Duval, B., Eaves, K.,
Egan, A., Escotto, M., Eugene, C., Evans, C.A., Falls, T., Fan, G.,
Fraser, C.M., Gabisi, A., Ganta, R., Garcia, A., Garner, T., Garza, M.,
Gebregeorgis, E., Geer, K., Gill, R., Grady, M., Guerra, W., Guevara, W.,
Gunaratne, P., Haaland, W., Hamil, C., Hamilton, C., Hamilton, K.,
Harvey, Y., Haves, A., Henderson, N., Hernandez, J.,
Hernandez, R., Hines, S., Hulgk, S., Hume, J., Idlabird, D., Jackson, A.,
Jacob, L., Jacob, L., Jiang, H., Johnson, B., Johnson, R., Jolivet, A.,
Karpathy, S., Kelly, S., Kelly, S., Khan, Z., King, L., Kovar, C.,
                                                                                                                    Karpathy, S., Kelly, S., Kelly, S., Khan, Z., King, L., Kovar, C., Kowis, C., Kraft, C.L., Lebow, H., Levan, J., Lewis, L., Li, Z., Liu, J., Longacre, S., Lopez, J., Lorensuhewa, L., Loulseged, H., Lozado, R. J., Lu, X., Ma, J., Lorensuhewa, L., Loulseged, H., Lozado, R. J., Lu, X., Ma, J., Lorensuhewa, L., Loulseged, H., Lozado, R. J., Lu, X., Ma, J., Maheshwari, M., Mahindartne, M., Mahmoud, M., Malloy, K., Mangum, A., Martin, K., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Meenen, E., Manyam, M., Moleod, M.P., McNeill, T.Z., Meenen, E., Milosavljevic, A., Miner, G., Minja, E., Montemayor, J., Moore, S., Milosavljevic, A., Miner, G., Minja, E., Montemayor, J., Murphy, M., Nair, L., Martin, S., Munidasa, M., Nurphy, M., Nair, L., Nankervis, C., Neal, D., Newton, N., Nundasa, M., Nurphy, M., Nair, L., Nankervis, C., Neal, D., Newton, N., Nouris, S., Parks, K., Nakeleneh, O., Okwuonu, G., Olarnpunsagoon, A., Pal, S., Parks, K., Pasternak, S., Paul, H., Perez, A., Perez, L., Pfannkoch, C., Plopper, F., Polindexter, A., Popovic, D., Primus, E., Pu, L.-L., Puzzo, M., Oliroz, J., Rachlin, E., Reeves, K., Regler, M.A., Reigh, R., Paster, M., Parks, K., Paster, M., Pa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               84821
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AC107604.4 GI:23266137
HTG: HTGS_PHASE2; HTGS_DRAFT; HTGS_ENRICHED
Reilly,B., Reilly,M., Ren,Y., Reuter,M., Richards,S., Riggs,F.,
Rives,C., Rodkey,T., Rojas,A., Rose,M., Rose,R., Ruiz,S.J.,
Sanders,W., Savery,G., Scherer,S., Scott,G., Shatsman,S., Shen,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Muzny, D. Marie., Metzker, M. Lee., Abramzon, S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleost
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rattus norvegicus (Norway rat)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AC107604 223885 bp DNA linear HTG 21-SEP-2002
Rattus norvegicus clone CH230-196K4, *** SEQUENCING IN PROGRESS
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AU183957(R0167),D46798(S11701),AU077610(E20630)
Similar to Arabidopsis thaliana chromosome5, At5g55530
unknown protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /gene="0J1060_D03.12"
38163. .39500
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /gene="0J1060_D03.12"
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94.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Gaps
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REFERENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (21-SEP-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
on Sep 21, 2002 this sequence version replaced gi:21737824.
The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequening reads assembled using Atlas (http://www.hgsc.bcm.tmc.edu/projects/rat/). As a result, the sequence may extend beyond the ends of the clone and there may be contigs that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence contigs will be indicated in the feature table.
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Submitted (23-JAN-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 223885)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Worley, K.C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              consists of 1 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submittor.

This sequence will be replaced
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
NOTE: This is a 'working draft' sequence. It currently
                                                                                                                                                                                                                                                                                                                                                                   the accession number will be preserved.

1 223885: contig of 223885 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                            by the finished sequence as soon as it is available and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Assembly program. Phrap; version 0.990329
Consensus quality: 212075 bases at least Q40
Consensus quality: 215656 bases at least Q20
Consensus quality: 214644 bases at least Q20
Estimated insert size: 222767; sum-of-contigs estimation
Quality coverage: 5x in Q20 bases; sum-of-contigs estimat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Center project name: GPUL Center clone name: CH230-196K4
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                                         1866.
                                                                                                                                                                                                                                      /organism="Rattus norvegicus"
/mol_type="genomic DNA"
                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
/note="clone_boundary
                                                           /note="wgs_end_extension
clone_end:Sp6"
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DEFINITION ACCESSION
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                                                   Bryant, N., Bladar, U., Carter, K., Cavazos, I., Ceasar, H., Center, A., Cardenas, V., Carter, K., Cavazos, I., Ceasar, H., Center, A., Chank, V., Chen, R., Chen, R., Chen, Y., Chen, Z., Chu, J., Chavez, D., Chen, G., Chen, R., Chen, Y., Chen, Y., Chen, Z., Chu, J., Chavez, D., Cockrell, R., Cox, C., Coyle, M., Cree, A., D'Souza, L., Claveland, C., Cockrell, R., Cox, C., Coyle, M., Cree, A., D'Souza, L., Claveland, C., Denson, S., Darya, C., Ding, Y., Dinh, H., Divya, K., Dayala, M., Elgan, A., Escotto, M., Eugene, C., Evans, C.A., Falls, T., Fan, G., Egan, A., Escotto, M., Eugene, C., Evans, C.A., Falls, T., Fan, G., Egan, A., Escotto, M., Eugene, C., Evans, C.A., Falls, T., Fan, G., Egan, A., Escotto, M., Eugene, C., Evans, C.A., Garrer, T., Garza, M., Gebregoorgis, E., Geer, K., Gill, R., Grady, M., Guerra, W., Guevara, W., Gunaratne, P., Haaland, W., Hamil, C., Hamilton, C., Hamilton, K., Hernandez, S., Haldun, S.L., Hodgson, A., Hernandez, J., Hernandez, S., Hulyk, S., Hune, J., Idlebird, D., Jackson, A., Hollins, B., Howells, S., Hulyk, S., Hune, J., Idlebird, D., Jackson, A., Jackson, A., Jackson, A., Jackson, A., Jackson, L., Jacob, L., Jiang, H., Johnson, B., Johnson, R., Jolivet, A., Karpathy, S., Kelly, S., Kelly, S., Khan, Z., King, L., Kovar, C., Kowls, C., Kraft, C.L., Lebow, H., Levan, J., Lewis, L., Li, Z., Liu, J., Liu, J., Liu, Y., London, P., Longacre, S., Lopez, J., Liu, J., Mahshari, M., Mahindarthe, M., Mahmoud, M., Malloy, K., Mangum, A., Mangum, B., Mapua, P., Martin, K., Martin, R., Martinez, E., Motemayor, J., Moore, S., Milosar, M., Mahmoud, M., Malloy, K., Mangum, A., Nankervis, C., Neaton, M., Nauris, S., Munidasa, M., Murphy, M., Nair, L., Perez, A., Perez, L., Pfannkoch, C., Paul, H., Perez, A., Perez, L., Pfannkoch, C., Pilmus, E., Photo, C., Revers, K., Regier, M. A., Reigh, R., Pelally, M., Reilly, M., Reilly, R., Reilly, R., Reilly, R., Reilly, R., Reigh, R., Reigh, R., Reigh, R., Reigh, R., Reilly, R., Reilly, R., Reigh, R., Reigh, R., Reigh, R., Reigh, R., Reigh, R., Reigh, 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rattus norvegicus (Norway rat)
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Baldwin,D., Bandaranaike,D., Barber,M., Barnaike,M., Bandaranaike,D., Barber,M., Barnaike,M., Barnaike,
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Rives,C., Rodkey,T., Rojas,A., Rose,M., Rose,R., Ruiz,S.
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222550. .223885
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                                    Reilly, M., Ren, Y., Reuter, M., Richards, S., Riggs, F.,
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On May 9, 2003 this sequence version replaced gi:2326554.
The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence only contigs will be indicated in the feature
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Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                        NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/cenbank.draft_data.html).

NOTE: This is a 'working draft' sequence. It currently consists of 1 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submittor.
                                                                                                                                                                                                                                         This sequence will be replaced by the finished sequence as soon as it is available and the accession number will be preserved.

1 236021: contig of 236021 bp in length.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (bases 1 to 236021)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Center clone name: CH230-4E17

Assembly program: Atlas;
Assembly program: Atlas;
Consensus quality: 218135 bases at least Q40
Consensus quality: 221412 bases at least Q20
Consensus quality: 223855 bases at least Q20
Estimated insert size: 229824; sum-of-contigs estimation
Quality coverage: 6x in Q20 bases; sum-of-contigs estimation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Center project name: GAUD Center clone name: CH230-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Web site: http://www.hgsc.bcm.tmc.edu/Contact: hgsc-help@bcm.tmc.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Center code: BCM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Center: Baylor College of Medicine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ----- Genome Center
                                                                                                         /organism="Rattus norvegicus"
/mol_type="genomic DNA"
                                                                                                                                                                                    1. .23602:
                                                                                                                                                                                                                   Location,
                                     /clone="CH230-4E17"
                                                                   /db_xref="taxon:10116"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Shvartsbeyn,A., Sisson,I., Sitter,C.D., Smajs,D., Sodergren,E., Song,X.-Z., Sorelle,R., Sosa,J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Project Information
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ACCESSION
VERSION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DEFINITION
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Best Local S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cardenas, V., Carter, K., Cavazos, I., Ceasar, H., Center, A., Chen, S., Chen, S., Chen, S., Chen, Y., Chen, Z., Chu, J., Clacko, J., Chavez, D., Chen, G., Chen, R., Chen, Y., Chen, Z., Chu, J., Clacko, J., Clavez, D., Cox, C., Cox, C., Coyle, M., Cree, A., D'Souza, L., Claved, M., L., Davis, C., Davy-Carroll, L., De Anda, C., Dederlch, D., Davila, M.L., Davis, C., Davy-Carroll, L., De Anda, C., Dederlch, D., Davila, M.L., Davis, C., Durbin, K., Duval, B., Eaves, K., Draper, H., Duyan-Rocha, S., Dunn, A., Durbin, K., Duval, B., Eaves, K., Egan, A., Escotto, M., Eugene, C., Evans, C.A., Falls, T., Fan, G., Farnandez, S., Finley, M., Flagy, N., Forbes, L., Foster, M., Foster, P., Fraser, C.M., Gabisi, A., Ganta, R., Garcia, A., Garner, T., Garza, M., Gebregeorgis, E., Geet, K., Gill, R., Grady, M., Guerra, W., Guevara, W., Gebregeorgis, E., Geet, K., Gill, R., Grady, M., Guerra, W., Guarathe, P., Haaland, W., Hamil, C., Hamilton, C., Hamilton, K., Harvey, Y., Havlak, P., Hawes, A., Henderson, N., Hernandez, J., Hernandez, J., Jiang, H., Johnson, B., Johnson, R., Jolivet, A., Karpathy, S., Kelly, S., Khan, Z., King, L., Kovar, C., Karpathy, S., Kraft, C.L., Lebow, H., Levan, J., Lewis, L., Li, Z., Liu, J., King, L., Kovar, C., Li, J., Li
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            74712 GTCAAAAAACGTTGTGTCC 74694
                                             Liu, J. Liu, W., Liu, Y., London, P., Longacre, S., Lopez, J.,
Lorensuhewa, L., Loulseged, H., Lozado, R. J., Lu, X., Ma, J.,
Lorensuhewa, L., Loulseged, H., Lozado, R. J., Lu, X., Ma, J.,
Mahamud, M., Malloy, K., Mangum, A.,
Mangum, B., Mapua, P., Martin, K., Martin, R., Martinez, E.,
Mangum, B., Mapua, P., Martin, K., Martin, R., Martinez, E.,
Mangum, B., Mapua, P., Martin, K., Martin, R., Martinez, E.,
Mawhiney, S., McLeod, M.P., McMeill, T. Z., Meenen, E.,
Miner, G., Minja, E., Montemayor, J., Moore, S.,
Minorgan, M., Morris, K., Morris, S., Munidasa, M., Murphy, M., Nair, L.,
Mankervis, C., Neal, D., Newton, N., Nguyen, N., Norris, S.,
Mankervis, C., Neal, D., Newton, N., Nguyen, N., Norris, S.,
Mankervis, C., Neal, D., Newton, N., Nguyen, N., Norris, S.,
Mankervis, C., Neal, D., Newton, N., Nguyen, N., Norris, S.,
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Mankervis, C., Neal, D., Newton, N., Nguyen, N., Norris, S.,
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Mankervis, C., Neal, D., Newton, N., Nguyen, N., Norris, S.,
Mankervis, C., Neal, D., Newton, N., Nguyen, N., Norris, S.,
Mankervis, C., Neal, D., Newton, N., Nguyen, N., Norris, S.,
Mankervis, C., Neal, D., Newton, N., Nguyen, N., N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Muzny, D. Marie., Metzker, M. Lee., Abramzon, S., Adams, C., Alder, J., Allen, C., Allen, H., Alsbrooks, S., Amin, A., Anguiano, D., Anyalebechi, V., Aoyagi, A., Ayodeji, M., Baca, E., Baden, H., Baldwin, D., Bandaranaike, D., Barber, M., Barnstead, M., Benahmed, F. Biswalo, K., Blair, J., Blankenburg, K., Blyth, P., Brown, M., Bryant, N., Buhay, C., Burch, P., Burrell, K., Calderon, E., Cardons, C., Burch, P., Burrell, K., Calderon, E., Cardons, C., Cardo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 GTCAAAAACCGTTGTGTCC 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rattus norvegicus (Norway rat)
Rattus norvegicus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AC105688 236062 bp DNA linear HTG 21-SEP-2002
Rattus norvegicus clone CH230-11H4, *** SEQUENCING IN PROGRESS ***,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_ENRICHED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AC105688.3 GI:23264260
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complement(229315. .230090)
/note="clone_boundary
clone_end:T7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="wgs_end_extension
clone_end:Sp6"
5478. .6115
/note="clone_boundary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      end_sequence:BH305226*
232901. .236021
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clone_end:T7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            site:EcoRI
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94.7%;
Okwuonu,G.,
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Pred. No. 1.
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       Olarnpunsagoon, A.,
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       Pal,S., Parks,K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0;
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                                                                                          source
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Baylor Plaza, Houston, TX 77030, USA on Sep 21, 2002 this sequence version replaced gi:21743898. The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequening reads assembled using Atlas (http://www.hgsc.bcm.tmc.edu/projects/rat/). As a result, the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      sequence may extend beyond the ends of the clone and there may be contigs that consist entirely of whole genome shotunn sequence reads. Both end sequences and whole genome shotunn sequence contigs will be indicated in the feature table.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (21-SEP-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rat Genome Sequencing Consortium Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Yu,F., Zhang,J., Zhou,J., Zhou,X., Zhao,S., Dunn,D., von Niederhausern,A., Weiss,R., Smith,D.R., Holt,R.A., Smith,H.O., Weinstock,G. and Gibbs,R.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Puazo,M., Quiroz,J., Rachlin,E., Reeves,K., Regier,M.A., Reigh,R., Reilly,B., Reilly,M., Ren,Y., Reuter,M., Richards,S., Riggs,F., Rives,C., Rodkey,T., Rojas,A., Rose,M., Rose,R., Ruiz,S.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unpublished
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                                                                                                                                                                                                                                                                                                                                                                        NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html)
NOTE: This sequence may represent more than one clone.
NOTE: This is a 'working draft' sequence. It currently consists of 2 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence
                                                                                                                                                                                                                                                                                                                                      as soon as it is available and the accession number will
                                                                                                                                                                                                                                                                                               be preserved
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Assembly program: Phrap; version 0.990329
Consensus quality: 200479 bases at least Q40
Consensus quality: 204791 bases at least Q30
Consensus quality: 207411 bases at least Q30
Consensus quality: 207411 bases at least Q20
Estimated insert size: 251580; sum-of-contigs estimation
Quality coverage: 3x in Q20 bases; sum-of-contigs estimation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Web site: http://www.hgsc.bcm.tmc.edu/Contact: hgsc-help@bcm.tmc.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Center project name: GNND
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Center code: BCM
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                                          /organism="Rattus norvegicus"
                                                                                              1. .236062
                                                                                                                            5 236062: contig of 1738 bp in length Location/Qualifiers
/mol_type="genomic DNA"
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                                                                                                                                                                                                              234224: contig of 234224 bp in length 234324: gap of unknown length
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AJ414153.1 GI:15980576
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Prentice,M.B., Sebaihia,M., James,K.D., Churcher,C., Mungall,K.L.,
Baker,S., Basham,D., Bentley,S.D., Brooks,K., Cerdeno-Tarraga,A.M.,
Chillingworth,T., Cronin,A., Davies,R.M., Davis,P., Dougan,G.,
Chillingworth,T., Cronin,A., Davies,R.M., Davis,P., Dougan,G.,
Reltwell,T., Hamlin,N., Holroyd,S., Jägels,K., Leather,S.,
Karlyshev,A.V., Moule,S., Oyston,P.C.F., Quail,M., Rutherford,K.,
Simmonds,M., Skelton,J., Stevens,K., Whitehead,S. and Barrell,B.G.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Simmonds,M., Skelton,J., Stevens,K., Whitehead,S. and Barrell,B.G Genome sequence of Yersinia pestis, the causative agent of plague Nature 413 (6855), 523-527 (2001)
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                                                                                                                                                                                                                                                                                                             (URL,
                                                                                                                                                                                                                                                                                                                                                                                                         sequencing team, Sanger
Hinxton, Cambridge CB10
                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (04-OCT-2001) Submitted on behalf of the Yersinia sequencing team, Sanger Centre, Wellcome Trust Genome Campus,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Enterobacteriaceae; Yersinia.
1 (bases 1 to 258050)
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Yersinia pestis CO92
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                                                                                                                                                                                                                                                                                                                                                         Details of Y. pestis sequencing at the Sanger Centre are available
                                                                                                                                                                                                                                                                                                                                                                                     Notes
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Parkhill, J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
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                                                                                                                                                                                                                                                                                                                                      the world wide web.
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                                                                                                                                                                                                                                                                                                             http://www.sanger.ac.uk/Projects/Y_pestis/)
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complement(231465. .2
/note="clone_boundary
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179267. .180672
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/note="no significant database hits"
/codon_start=1
                                                                                                                                                                                          /mol_type="genomic
/strain="CO92"
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/clone="CH230-11H4"
                                               /gene="YP02590"
                                                                                              /gene="YP02590"
                                                                                                                                        /note="biovar: Orientalis"
                                                                                                                                                                      /db_xref="taxon:214092"
                                                                                                                                                                                                                 /organism="Yersinia pestis
/mol_type="genomic DNA"
                                                                                                                                                                                                                                                                                         ocation/Qualifiers
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94.7%;
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Pred. No. 1.7e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                         parkhill@sanger.ac.uk
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misc_feature
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                                                                                                                                                                                                                                                         /note="one of 9 probable for YPO2592 by TMHMM2.0" complement(1497. .1547)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note-"one of 9 probable for YPO2592 by TMHMM2.0" complement(1206. .1262)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="one of 9 probable transmembrane helices for YPO2592 by TMHMM2.0" complement(1101. .1186)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               complement(972. .1937)
/gene="YPO2592"
complement(972. .1937)
/gene="YPO2592"
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/gene="YPO2591"
complement(608. .790)
/gene="YPO2591"
                                                                                                                                                complement(1569. .1634)
/gene="YPO2592"
                                                                                                                                                                                                                                                                                                                                                   complement(1401. .1451)
/gene="YPO2592"
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QYERLWTWIEYYMTGRELCSRICQKWTKLPKVRLAAKLLLLPTSISMYYYESEMSIYV
YKTVNASYELDNEHVLVLSLCLEVIEDNEDTQYEWIKKTLAYISPSMIGVYILHDGIE
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/translation="MRNVGLHALKTLSCFSAVTFYSASKTCTEQCFLSGEVMGVLYFL
SIIATPLFFMIIGYIDSNDKIDQKDIFRKLKSIITIIFWNVLFYFINEDGFKRGYFL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /product="putative membrane protein"
/protein_id="CAC92835.1"
/db_xref="GI:15980579"
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TTIEVHITQVAYLISV"
/note="one of 9 probable transmembrane helices for YPO2592 by TMHMM2.0"
                                                                                               note="one of 9 probable for YPO2592 by TMHMM2.0"
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for YPO2592 by TMHMM2.0"
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for YPO2592 by TMHMM2.0"
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for YPO2592 by TMHMM2.0"
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/protein_id="CAC92834."
                                                   /gene="YP02592"
                                                                                                                                                                                                                                                    /gene="YP0259;
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/protein_id="CAC92833.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /gene="YP02592"
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                                                                                                                                                                                                                                                                                           /note="Similar to Escherichia coli probable cold shock protein CspE SW.CSPE ECOLI (P36997) (68 aa) fasta scores: E(): 1e-25, 94.1% id in 68 aa, and to Vibrio cholerae hypothetical protein TR:AAC73388 (EMBL.AE098260) (69 aa) fasta scores: E(): 3.1e-26, 94.2% id in 69 aa. Similar to YPO1746 (84.1% identity in 69 aa overlap), YPO1655 (83.3% identity in 66 aa overlap), YPO3644 (73.6% identity in 72 aa overlap), YPO3643 (72.2% identity in 72 aa overlap), YPO3643 (73.2% identity in 72 aa overlap), YPO3669 (63.9% identity in 72 aa, verlap) and YPO398
                                                                     /db_xref="Sptrembl:Q8zDH3"
/translation="MSKIKGSVKWFNESKGFGFITPEDGSKDVFVHFSAIASNGFKTL
AEGQRVEFEITNGAKGPSAANVIAI"
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/gene="YPO2594"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="Similar to Salmonella typhimurium fimbriae W protein FimW SW:FIMM_SALTY (P37928) (198 aa) fasta score(): 0.0066, 21.9% id in 178 aa, and to C-terminus of Erwinia amylovora activator of exopolysaccharide synthesis, RcsB TR:P96320 (EMBL:Y09848) (215 aa) fasta scores: E(): 0.0003, 43.7% id in 71 aa"
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/genė="YPO2592"
                       4060. .4260
/gene="cspE"
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AFYSADVIFIGVDEFSFFEALKRLDKTPAEADVFLICDARLNSFLQGIPRFSDVTMIF
REDSLETVSNKIATYFKRKFRGFKDNLIERKTAKVLHLVSSERQYLTPNENIVLKLFN
EGFSGGDIARILKKSEKTVSGQKRSAMKKLGARTDVELIKMFMFK"
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for YPO2592 by TMHMM2.0"
2360. .2977
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /translation="MIKKGAEVTFEPTTNTKGLSAFAVKVAIESKYIFIANERIKLTS
IKSFNTFTKEVPAQAEVDKANTILSVNLLMNKIRPQEEDISEKTIPLKMLSITTFQNV
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/protein_id="CAC92836.1"
/db_xref="GI:15980580"
note="Pfam match to entry PF00313 CSD, 'Cold-shock'
                                                                                                                                             /protein_id="CAC92838.
/db_xref="GI:15980582"
                                                                                                                                                                                                                                                                         (53.6% identity in 69 aa
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/protein_id="CAC92837.1
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                                                                                                                                                                                                 'product="putative cold shock
                                                                                                                                                                                                                        transl_table=11
                                                                                                                                                                                                                                                    codon_start=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         note="synonym:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        db_xref="GI:15980581"
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RESULT 15
AF234529
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AUTHORS
TITLE
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E05251
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OC Artificial ge
OC Human papillo
PN JP 193192200
PN JP 193192200
PN JP 19319290
PF 19-AUG-1991 J
PR 20-AUG-1990 J
PR 20-AUG-1990 J
PR 20-AUG-1990 J
PI OKAZAWA KAZUH
FUKUSHIMA MICHIO,
PI FUJINAGA KEI
PC C12Q1/70,C12Q
CC strandedness:
CC topology: Lin
CC hypothetical:
CC anti-sense: N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               artificial sequences.

1 (bases 1 to 20)

Okasawa,K., Shimada,M., Katou,I., Fukushima,M.

DETECTION OF HUMAN PAPILLOMA VIRUS

Patent: JP 1993192200-A 21 03-AUG-1993;

TAKARA SHUZO CO LTD

TAKARA SHUZO CO LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 TGTCAAAAACCGTTGTGTC 19
AF234529
AF234529.1
                                       Human papillomavirus type
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      synthetic construct
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                                                         AF234529
                                                                                                                                           TGTCAAAAACCGTTGTGTCC
                                                                                                                              TGTCAAAGACCTTTGTGTCC 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Artificial gene
Artificial sequence; G
Human papillomavirus
JP 1993192200-A/21
03-AUG-1993
                                                                                                                                                                                                                                                                                                                                                                                        FUJINAGA KEI
C12Q1/70,C12Q1/68;
strandedness: Single;
                                                                                                                                                                                                                                                                                                                                                                                                                                               19-AUG-1991 JP 1991230839
20-AUG-1990 JP 90P 217067
OKAZAWA KAZUHIDE, SHIMADA MASAMITSU, KATOU IKUNOSHIN, PI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           of DNA sequence of
                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                  anti-sense: No.
                                                                                                                                                                                                                                                                                                                                                             topology: Linear;
hypothetical: No;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /gene="crcB"
/note="synonym: YPO2596"
complement(4686. .5069)
                                                                                                                                                                                                                                                           /organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630" 7 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="PS00352 'Cold-shock' DNA-binding domain signature."
complement(4686. .5069)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /gene="crc8"
                                                                                                                                                                                                                                                                                                                                 ocation/Qualifiers
GI:7331167
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94.7%;
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Pred. No. 3.1e+02;
0; Mismatches 2;
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Pred. No. 1
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Human papillomavirus 33.
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                                          bp r
strain
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1.7e+02;
hes 1;
                                        DNA linear
E6HK1 E6 prote
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                                     lnear VRL 28-MAR-2000
protein gene, complete
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KEYWORDS
SOURCE
ORGANISM
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REFERENCE
AUTHORS
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Search completed: August
Job time : 995 secs
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                                                             316 TGTCAAAGACCATTGTGTCC 335
                                                                             1 TGTCAAAAACCGTTGTGTCC
                                                                                                                            18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (15-FEB-2000) Department of Microbiology, The Chinese University of Hong Kong, Prince of Wales Hospital, Shatin, NT.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 (bases 1 to 450)
Chan, P.K.S., Lam, C.W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 (bases 1 to 450)
Chan, P.K.S., Lam, C.W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human papillomavirus type 58
Human papillomavirus type 58
Viruses; dsDNA viruses, no Rb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cheng, A.F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cheng, A.F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      papillomavirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nucleotide sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cancerous lesions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Papillomavirus.
                                                                                                                                             Similarity
                                                                                                                                                                                                          158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Kong
                                                                                                                            Conservative
                                                                                                                                                                                                       /translation="MFQDAEEKPRTLHDLCQALETSVHEIELKCVECKKTLQRSEVYD FVFADLRIVYRDGHFAVCKVCLRLLSKISEYEHYNYSLYGDTLEQTLKKCLNEILIR CIICQRPLCEDEKKRHVDLNKREHNISGRWTGRCAVCWRPRRRQTQV" 128 t
                                                                                                                                                                                                                                                                                                                                                                              /country="China"
/note="from cervical scrape of squamous cell carcinoma of the
                                                                                                                                                                                                                                                                                                                                     p53-binding"
                                                                                                                                                                                                                                                                    /codon_start=1
/product="E6 protein"
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                                                                                                                                                                                                                                                                                                                                                  /note="oncoprotein; transforming;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Human papillomavirus type 58"
/mol_type="genomic DNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                'db_xref="taxon:10598"
                                                                                                                                                                                                                                                                                                                                                                                                                                             solate="QEH61"
              23,
                                                                                                                                         84.0%;
90.0%;
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              2003, 11:11:33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      variation of the E6 gene of human 58 from Chinese women with normal
                                                                                                                            0
                                                                                                                                         Score 16.8; DB 14
Pred. No. 3.2e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Li,W.H.,
                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RNA stage; Papillomaviridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Chan, M.Y.M.,
                                                                                                                                                          DB 14;
                                                                                                                                                                                                                                                                                                                                                                                  patient with invasive cervix"
                                                                                                                                                          Length
                                                                                                                            Indels
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                                                                                                                                                           450;
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                                                                                                                            Gaps
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Title: Perfect score: Sequence:

US-09-927-585A-1 20 1 tgtcaaaaaccgttg

tgtcaaaaaccgttgtgtcc

20

Run on: OM nucleic

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nucleic search, using sw model

GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.

Scoring table:

IDENTITY\_NUC
Gapop 10.0 , Gapext 1.0

2552756 seqs, 1349719017 residues

Minimum Maximum

DB BCD

length: 0 length: 2000000000

Total number of hits satisfying chosen parameters:

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 s

summaries

Database

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16 16

AAH70910 AAN91602 ABQ76303 AAF25493 AAF25498 AAH41227

S. cerevisiae BAX-Human cervical can Partial nucleotide

Nucleotide

sequenc

Pyrococcus abyssi Nucleotide sequenc

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August 23, 2003, 05:06:07; Search time 206.5 Seconds (without alignments) 261.447 Million cell updates/sec
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RESULT 1
AAQ48566
ID AAQ48566
AC AAQ4
XX 22-F
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human papilloma virus; HPV; E6; E7; benign; malignant; probe; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HPV E6/7 region probe.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      22-FEB-1994
                                                                                                                                                                                                                                                                                                                                                                                                                            03-AUG-1993.
Disclosure; Page 15; 18pp; Japanese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             JP05192200-A
                                                                                       Detecting benign and/or malignant human papilloma virus - by detecting DNA sequence of E6 and/or E7 region of human papilloma
                                                                                                                                                                                     WPI; 1993-277497/35.
                                                                                                                                                                                                                                         (TAKI ) TAKARA SHUZO CO LTD
                                                                                                                                                                                                                                                                                                          20-AUG-1990;
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HPV16 E6 SiRNA der Human papilloma vi Mammalian vestibul Mammalian vestibul
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ed. No. is the number greater than is derived by a Score 20 20 20 18.4 18.4 16.8 16.8 is the number of results predicted by chance to have a ater than or equal to the score of the result being printed, rived by analysis of the total score distribution. Query Match 100.0 100.0 100.0 92.0 92.0 84.0 84.0 Length 20 20 20 20 20 20 1023 20 540 В ij AAQ48566 AAS18612 ABZ75144 AAQ48556 AAQ48575 AAQ48560 ABT11435 SUMMARIES HPV E6/7 region pr Middle-high hazard Oncogenic HPV region pr HPV E6/7 region pr HPV E6/7 region pr Yeast selected int Selected Interacti Description

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                                                                                                        The invention describes a novel method of identifying viral DNA of human papililomavirus (HPV) in cellular material collected from an individual. The method comprises extracting DNA from the cellular material, amplifying the DNA by using a polymerase, and identifying sequences of the HPV genome using an identifying reagent. The presence of HPV in cells is now based on identification of a nucleotide sequence in the II identify the presence of HPV virus in every stage of infection and to distinguish between virus strains having low hazard and virus strains region of middle-high hazard. This is the primer used to identify the E6 hazard HPV strains in infected cells, described in
                                                                                    Sequence
                                                                                                                                                                                                                                                                            Claim
                                                                                                                                                                                                                                                                                                   Identifying viral DNA of human papilloma virus in cellular material collected from an individual, by using polymerase and identifying sequences complementary to regions E of the viral genome using a
                                                                                                                                                                                                                                                                                                                                                                                  Perseu
                                                                                                                                                                                                                                                                                                                                                                                                 (BIOA-) BIOANALISI CENT SUD DI PERSEU SINIBLADO
                                                                                                                                                                                                                                                                                                                                                                                                                          05-MAY-2000; 2000IT-MO00091
                                                                                                                                                                                                                                                                                                                                                                                                                                                 02-MAY-2001; 2001WO-IB00771
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15-NOV-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human papillomavirus; HPV; early gene; E6; PCR primer; middle-high hazard; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human papillomavirus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    probe is used to detect benign and/or malignant human papilloma us. The probe binds to the E6 and/or E7 region of the virus.
           1 TGTCAAAAACCGTTGTGTCC 20
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                                                                                                                                                                                                                                                                       Page 12; 17pp; English.
Similarity
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The invention relates to a method for preparing a stabilised reaction CC mixture which contains at least one enzyme and which is at least CC maixture which contains at least one enzyme and which is at least CC mixture which containing an enzyme and a three-component stabiliser CC solution mixture containing an enzyme and a three-component stabiliser CC solution mixture containing an enzyme and a three-component stabiliser CC three-component stabiliser solution used in the method comprises an CC agent which protects against dessication, an inhibitor of condensation CC groups, and an inert polymer that forms a mesh structure that inhibits the method comprises and CC acid manipulations such as amplification, sequencing, hybridisation CC used as "ready-to-use" mixtures for performing a wide range of nucleic and/or restriction analysis, e.g., for the diagnostic detection of CC and/or restriction analysis, e.g., for the diagnostic detection of CC and/or restriction analysis, e.g., for the diagnostic detection of CC components needed to perform a particular reaction, already deposited in CC areaction vessel, which eliminates the need for multiple additions crepeatability and reliability. The dried reaction, thereby improving transported and stored at ambient temperature without significant loss of activity, and are suitable for "not start" reactions. Sequences CC amplify regions of human papillomavirus (HPV) genomes in order to characterise their type. Primers ABZ75142-ABZ75143 are PCR primers used CC characterise their type. Primers ABZ75143 are used to amplify a 250 bp
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Marin Alberdi MD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           oncogenic type; E6-E7; Page 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human
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type 18.
type 31.
type 33.
type 35.
type 52b.
type 58.
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RESULT 5
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                                                                                                                                                                                        Query Match
Best Local S
Matches 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
          Synthetic
                           Human papilloma virus; HPV;
                                                                                                                                                                                                                                             The probe is used to detect benign and/or malignant human papilloma virus. The probe binds to the E6 and/or E7 region of the virus.
                                                                                                                                                                                                                                                                         Disclosure; Page 14; 18pp; Japanese.
                                                                                                                                                                                                                                                                                                    Detecting benign and/or malignant human papilloma virus - by detecting DNA sequence of E6 and/or E7 region of human papilloma
                                              HPV E6/7 Genomic region.
                                                                  22-FEB-1994
                                                                                    AAQ48575;
                                                                                                      AAQ48575 standard; DNA; 1023 BP
                                                                                                                                                                                                                             Sequence 20 BP; 4 A; 5 C; 5 G; 6 T; 0 other;
                                                                                                                                                                                                                                                                                                                                   WPI; 1993-277497/35
                                                                                                                                                                                                                                                                                                                                                                                         19-AUG-1991;
                                                                                                                                                                                                                                                                                                                                                                                                            03-AUG-1993
                                                                                                                                                                                                                                                                                                                                                                                                                               JP05192200-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human papilloma virus; HPV;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HPV E6/7 region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAQ48556;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAQ48556 standard; DNA; 20 BP
                                                                                                                                                                                                                                                                                                                                                     (TAKI ) TAKARA SHUZO CO LTD
                                                                                                                                                                                                                                                                                                                                                                        20-AUG-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           22-FEB-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        region designated E6-E7 from oncogenic HPV types only.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 20 BP; 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local
                                                                                                                                                                                         l Similarity
19; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 TGTCAAAAACCGTTGTGTCC 20
|||||||||||||||||||||||
1 TGTCAAAAACCGTTGTGTCC 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 th 100.0%; Score 20; DB 25; Similarity 100.0%; Pred. No. 2.3; 20; Conservative 0; Mismatches 0,
                                                                                                                                                   TGTCAAAGACCGTTGTGTCC 20
                                                                                                                                                              TGTCAAAAACCGTTGTGTCC 20
                                                                                                                                                                                         Conservative
                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                       90JP-0217067
                                                                                                                                                                                                                                                                                                                                                                                         91JP-0230839
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      probe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; 5 C; 4 G; 6 T; 0 other;
                                                                                                                                                                                                92.0%;
                          benign; malignant;
                                                                                                                                                                                         0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 E6; E7; benign; malignant; probe; ss
                                                                                                                                                                                                Score 18.4;
Pred. No. 14;
                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                          DB 14;
                                                                                                                                                                                       ۲,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0;
                            E6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 20;
                                                                                                                                                                                                          Length
                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                            E7;
                                                                                                                                                                                                          20;
                                                                                                                                                                                       0;
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                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                       0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0;
                                                                                                                                                                                                                                                      RESULT 6
AAQ48560
₽
                                                                                                                                                                                                                                                                                                                                                                       SXCCCCXXX
                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                               Probes
      Detecting benign and/or malignant human papilloma virus detecting DNA sequence of E6 and/or E7 region of human pap
                                                                                                             03-AUG-1993.
                                   WPI; 1993-277497/35.
                                                     (TAKI ) TAKARA SHUZO CO
                                                                        20-AUG-1990;
                                                                                                                               JP05192200-A.
                                                                                                                                                 Synthetic.
                                                                                                                                                                   Human papilloma virus; HPV; E6;
                                                                                                                                                                                     HPV E6/7 region probe
                                                                                                                                                                                                          22-FEB-1994
                                                                                                                                                                                                                            AAQ48560;
                                                                                                                                                                                                                                              AAQ48560 standard;
                                                                                                                                                                                                                                                                                                                                                                     Sequence 1023 BP; 355 A; 170 C; 227 G;
                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 1; Page 16-17; 18pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Detecting benign and/or malignant human papilloma virus - b detecting the DNA sequence of E6 and/or E7 region of human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1993-277497/35.
P-PSDB; AAR40919, AAR48202.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20-AUG-1990;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CDS
                                                                                          19-AUG-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     19-AUG-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           JP05192200-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (TAKI ) TAKARA SHUZO CO
                                                                                                                                                                                                                                                                                           565 TGTCAAAAACCGCTGTGTCC 584
                                                                                                                                                                                                                                                                                                      1 TGTCAAAAACCGTTGTGTCC 20
                                                                                                                                                                                                                                                                                                                                l Similarity
19; Conserv
                                                                                                                                                                                                                                                                                                                                                                                               were designed to detect benign and/or malignant human papilloma The probes bind to the E6 and/or E7 region of human papilloma
                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                Conservative
                                                                        90JP-0217067
                                                                                           91JP-0230839
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   90JP-0217067
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     91JP-0230839
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /*tag= a
/label= ORF-1
/note= "E6 reg
702..99%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
250..696
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /label= ORF-2
/note= "E7 region"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 '*tag=
                                                                                                                                                                                                                                              DNA;
                                                                                                                                                                                                                                                                                                                                         92.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ۲
                                                                                                                                                                                                                                               20
                                                     LTD
                                                                                                                                                                                                                                              ВP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  region"
                                                                                                                                                                                                                                                                                                                                0
                                                                                                                                                                                                                                                                                                                                         Score 18.4;
Pred. No. 18
                                                                                                                                                                  E7; benign; malignant; probe;
                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                           18;
                                                                                                                                                                                                                                                                                                                                                                     271 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                  DB 14;
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Length 1023; Indels

0;

Gaps

0

SS

ā papilloma

papilloma

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309 TGTGAAAAACCGTTGTTTCC

290

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RESULT 7
ABT11435/
ID ABT1
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Best Local S
Matches 18
                                   Query Match
Best Local S
Matches 18
                                                                                                                      The present invention relates to complexes between Saccharomyces cerevisiae Selected Interacting Domain (SID (RTM)) proteins and coding sequences. The protein complexes of S. cerevisiae are useful in drug development, in screening drugs or agents that modulate the interaction of proteins, for developing yeast strains with better secretion yield of protein, and in gene therapy. The protein complexes, polypeptides and polynucleotides are useful for preventing or treating Candida infection, cancer or neurodegenerative diseases in humans or animals. The present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The probe i
                                                                                                                                                                                                                                                          drug screening or development, secretion yield of protein, or infection or cancer) -
                                                                                                                                                                                                                                                                     New protein-protein complexes of Saccharomyces cerevisiae, useful in drug screening or development, for developing yeast strains with better secretion yield of protein, or in gene therapy (e.g. to treat Candida
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Yeast; protein-protein interaction; Selected Interacting Domain; SID (RTM); secretion yield; cancer; neurodegenerative disease; f cytostatic; neuroprotective; gene; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Saccharomyces cerevisiae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure;
                                                                                     Sequence
                                                                                                                                                                                                                                    Claim 7; Page 168;
                                                                                                                                                                                                                                                                                                                                                                                     (HYBR-) HYBRIGENICS
                                                                                                                                                                                                                                                                                                                                                                                                            16-FEB-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                    14-FEB-2002; 2002WO-EP02299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO200266504-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Yeast selected interacting domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10-DEC-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABT11435;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABT11435
                                                                                                                                                                                                                                                                                                                         2002-674913/72.
DB; ABJ11118.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18;
                                      l Similarity
18; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                     540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TGTCAAAAACCGTTGTGTCC 20
TGTCAAAAACCGTTGTGTCC
                                                                                                             is a coding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20 BP; 4 A; 5 C; 4 G; 7 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TGTCAAAGACCTTTGTGTCC 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         probe binds to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Page 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    used
                                                                                     BP;
                                                                                                                                                                                                                                                                                                                                                                                                             2001US-269266P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                     184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ç
                                                                                                                                                                                                                                    357pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            84.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        18pp;
                                                                                   Ą,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       detect benign and/or malignant human papilloma is to the E6 and/or E7 region of the virus.
                                                84.0%;
                                                                                                             sequence of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         540
                                                                                   116 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Japanese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ₽₽.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches
                                    0;
                                                Score 16.8;
Pred. No. 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 16.8;
Pred. No. 86;
                                                                                     113
                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                coding sequence SEQ
                                                                                   ი
:
                                                                                                             invention
                                                                                     127
                                                 .le+02;
                                                            DB 24;
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                                                                                   T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ٧,
                                                           Length 540;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length
                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ħ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             disease; fungicide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ő
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20;
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                                    0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  369
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                                    Gaps
                                    0
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RESULT 8
ABS62861/c
ID ABS62861 s
RESULT 9
AAH70910/
ID AAH7
XX AAH7
AC AAH7
XX 19-S
XX
DE Huma
XX . . .
XX
OS Homc
XX
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                                                                                                                                                                                                                                                    Query Match
Best Local S
Matches 18
                                                                                                                                                                                                                                                                                                                                      The invention relates to a complex between two interacting Saccharomyces cerevisiae polypeptides, comprising two Selected Interacting Domain (SID polypeptides as bait and prey proteins. A pharmaceutical composition comprising the complex is useful for preventing or treating Candida infection, cancer and neurodegenerative diseases in a human or animal, preferably in a mammal. This sequence represents DNA encoding a SID
                                                                                                                                                                                                                                                                                                                                                                                                                                                   New complex between two interacting bait and prey Saccharomyces cerevisiae polypeptides, useful for preventing or treating Candida infection, cancer or neurodegenerative diseases in a mammal -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Saccharomyces cerevisiae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               neurodegenerative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cytostatic; neuroprotective; Candida infection; gene therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Yeast; selected interacting
                                      Cervical cancer;
                                                                                                                                                                                                                                                                                                  Sequence 541 BP; 184 A; 116 C; 114 G;
                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 7; Page 80; 196pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2002-619165/66.
P-PSDB; ABG77247.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                25-JAN-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-AUG-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO200259255-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Selected Interacting Domain (SID) polynucleotide #58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        05-NOV-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABS62861;
                                                                                                                                       AAH70910 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (HYBR-) HYBRIGENICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       26-JAN-2001; 2001US-264577P
                                                               Human cervical
                                                                                       19-SEP-2001
                                                                                                               ААН70910;
                                                                                                                                                                                                                                                                                                                            polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Legrain
                                                                                                                                                                                                    310
                                                                                                                                                                                                                                                     l Similarity
18; Conserv
                                                                                                                                                                                                    TGTGAAAAACCGTTGTTTCC 291
                                                                                                                                                                                                                            TGTCAAAAACCGTTGTGTCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       standard; DNA;
                                                                                                                                                                                                                                                                                                                             of the invention.
                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2002WO-EP01350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first
                                                             cancer marker nucleic acid 2184.
                                    cytostatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  disease.
                                                                                                                                        cDNA; 766
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       entry)
                                                                                                                                                                                                                                                                84.0%;
90.0%;
                                                                                      entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        541
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         domain; SID; gene;
                                                                                                                                                                                                                                                     0;
                                      pre-malignant condition;
                                                                                                                                                                                                                                                                  Score 16.8;
Pred. No. 1.
                                                                                                                                                                                                                            20
                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                      127 T; 0 other;
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                                                                                                                                                                                                                                                                              DВ
                                                                                                                                                                                                                                                                              24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ds; antifungal; cancer;
                                                                                                                                                                                                                                                                              Length
                                                                                                                                                                                                                                                       Indels
                                      gene
                                      therapy;
                                                                                                                                                                                                                                                     0;
                                                                                                                                                                                                                                                     Gaps
                                       SS
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RESULT 10
AAN91602
ID AAN91
XX AAN91
AC AAN91
XX Parti
DT 17-JU
XX Parti
DE type
XX Human
XW Cellu
OS Human
XX W089(
XX W089(
XX OS-SI
XX OS-SI
XX OS-SI
XX OS-SI
XX WFI
PR O2-OX
XX PA (MICI
XX WPI;
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                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local
                                                                                                                                                                        Human papilloma cellular smear;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       polypeptides are useful: to assess if a patient is afflicted with cervical cancer or has a pre-malignant condition; to monitor the progression of cervical cancer or a premalignant condition in a patient; and to select and/or assess the efficacy of a compound or therapy for inhibiting cervical cancer in a patient. The nucleic acids may also be
                     Schwartz DE,
                                                                02-OCT-1987;
                                                                                    30-SEP-1988;
                                                                                                          06-APR-1989
                                                                                                                             WO8902934-A.
                                                                                                                                                    Human
                                                                                                                                                                                                        Partial nucleotide sequence type 33 (HPV-33).
                                                                                                                                                                                                                                         17-JUL-1990
                                                                                                                                                                                                                                                              AAN91602;
                                                                                                                                                                                                                                                                                   AAN91602 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 766 BP; 197 A; 158 C; 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to novel genes (AAH68727-AAH73383) cervical cancer with cytostatic activity. The nucleic ac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            08-DEC-1999;
21-DEC-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Schlegel R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      14-MAR-2000;
12-MAY-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            08-DEC-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 14-JUN-2001
                                           (MICR-) MICROPROBE CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO200142467-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                isolated nucleic acid for diagnosing and treating cervical cancer for assessing and detecting compounds for treating the cancer \boldsymbol{\cdot}
                                                                                                                                                                                                                                                                                                                                        734
                                                                                                                                                    papilloma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1; Page 462; 1051pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                for
                                                                                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                       TGTCAAAAGCCCTTGTGTCC
                                                                                                                                                                                                                                                                                                                                                           TGTCAAAAACCGTTGTGTCC 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                gene
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99US-0171350.
90US-0189315.
2000US-0203791.
2000US-0203791.
2000US-0220114.
                                                                                                                                                                                                                                                                                                                                                                                  Conservative
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                     Adams
                                                               87US-0103979
                                                                                    88WO-US03367
                                                                                                                                                                       virus; type 33; in cervical carcinoma
                                                                                                                                                                                                                                                                                                                                                                                                                                             therapy.
                                                                                                                                                    virus
                                                                                                                                                                                                                                                                                  DNA;
                                                                                                                                                                                                                                       entry)
                                                                                                                                                                                                                                                                                                                                                                                           84.0%;
90.0%;
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                                                                                                                                                                                                                                                                                                                                                                                           No. 1
                                                                                                                                                                                                                                                                                                                                                                                                                         244 T;
                                                                                                                                                                                                                 human
                                                                                                                                                                                                                                                                                                                                                                            1.1e+02;
2;
                                                                                                                                                                                  hybridisation assay;
                                                                                                                                                                                                                                                                                                                                                                                                     DB 22;
                                                                                                                                                                                                                                                                                                                                                                                                                           8 other;
                                                                                                                                                                                                                 papilloma virus
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ids and encoded
                                                                                                                                                                                                                                                                                                                                                                                                     766;
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                                                                                                                                                                                                                 (HPV)
                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                          Best Loc
Matches
                                                                                                       Query Match
                                                                                                                                                                     The patent is for a rapid in situ hybridisation assay for detecting and typing human papilloma virus (HPV) in non-frozen cellular smears fixed t a support in absence of aldehyde-based crosslinking reagents. The assay comprises: (1) combining nucleic acid in the sample with at least one detectable probe able to hybridise with 1 or more HPV types; and (2) detecting presence or absence of hybrid complexes. Opt. several probes are used, eg one for HPV types 6 and 11, associated with benign warts, and one for types 16, 18, 31, 33 and 35, associated with cervical cancer. The assay can differentiate between HPV types. It is esp. used as a secondary test. The probes can be synthesised or cloned.
                                                                                                                                                                                                                                                                                                                                                                                                                    Hybridisation test for human papilloma virus in comby reaction with long labelled probe specific for
                                                                                                                                                                                                                                                                                                                                                                     Disclosure;
                                                                                                                                                                                                                                                                                                                                                                                                  virus types, esp. for examining cervical smears
                                                                                       Local
1 TGTCAAAAACCGTTGTGTCC 20
                                                                     18; Conserv
                                                                                                                                        774 BP; 270
                                                                     Conservative
                                                                                     90.0%;
                                                                                                                                      A; 132 C; 163
                                                                                                                                                                                                                                                                                                                                                                   English.
                                                                     0
                                                                                   Score 16.8;
Pred. No. 1
                                                                     Mismatches
                                                                                                                                      G; 209 T; 0 other;
                                                                                       .1e+02;
                                                                                                       DB 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                        cell smears
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                                                                     Gaps
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                                                                     <u>.</u>.
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RESULT 11 ABQ76303/c vasotropic; vaccine apoptosis; fungal; S. cerevisiae ABQ76303 standard; 21-NOV-2002 ABQ76303; Bax-resistance; cytostatic; fungicide; immunosuppressive; virucide; tropic; vaccine; gene therapy; proliferative disorder; cancer; (first entry) BAX-associated yeast; infective cell death; CDNA; 3443 infection; cDNA fragment SEQ ВP autoimmune Ħ disease; 31.

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443

WO200264766-A2 Saccharomyces cerevisiae. neurodegeneration;

22-AUG-2002.

21-DEC-2001; 2001WO-EP15398

22-DEC-2000; 04-JAN-2001; 09-JAN-2001; ; 2000EP-0870318. ; 2001EP-0870002. ; 2001EP-0870003.

(JANC ) JANSSEN PHARM ₹

RH, Eberhardt Ţ, Luyten WHML, Reekmans

ŖJ;

2002-667002/71. DB; ABG93037.

New isolated nucleic acid representing a synthetic Bax gene, useful as medicament for treating, preventing and/or alleviating yeast or fungal infections or proliferative disorders, or for preventing apoptosis in certain diseases

Claim 36; Figure 1; 344pp; English.

This invention describes a novel nucleic acid representing a synthetic Bax gene. The Bax gene of the invention is useful for identifying Bax-resistant yeast or fungi, identifying, or obtaining and identifying. identifying

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RESULT 12
AAF25493/c
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Matches
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  The present
describes ad
                                                                                                      New polynucleotides encoding AMP deaminase or adenosine deaminase used e.g. for designing or identifying herbicides that inhibit the enzyme activities, and as probes for genetic or physical mapping -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Oryza sativa
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                                                               Claim 2; Page 53; 72pp; English
                                                                                                                                                                                                 P-PSDB;
                                                                                                                                                                                                                                                               Caspar T,
                                                                                                                                                                                                                                                                                                        (PION-)
                                                                                                                                                                                                                                                                                                                                                                          30-JUL-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AMP deaminase; adenosine deaminase; adenosine; transgenic plant;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ischaemia, diseases related with viral infections or neurodegenerations. This sequence represents a polynucleotide associated with the Bax gene described in the disclosure of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         inosine;
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                                                                                                                                                                                               2001-159866/16.
DB; AAB31953.
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PIONEER HI-BRED INT
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  adenosine o
                                                                                                                                                                                                                                                               Falco SC,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       202..312
/*tag= a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      of a rice AMP deaminase enzyme.
  encodes a deaminase.
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90.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "AMP deaminase"
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Pred. No. 1.
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n AMP c
These
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deaminase.
e enzymes c
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e. The specification convert adenosine to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2
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                      also
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The present sequence encodes an andenosine deaminase. The specification also describes adenosine deaminase. These enzymes convert adenosine to inosine. Mutations in these genes cause disruptions in then salvage and

Claim 2;

Page 67-68;

English

e.g. for designing activities, and as

probes for 72pp;

genetic

or

physical

mapping

New polynucleotides encoding AMP deaminase or adenosine deaminase used e.g. for designing or identifying herbicides that inhibit the enzyme

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RESULT 13
AAF25498/c
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Matches 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  nucleic acid fragments may be used to isolate cDNAs and genes encodi homologous proteins from the same or other plant species, and in polymerase chain reaction (PCR) protocols to amplify longer nucleic acid fragments encoding homologous genes from DNA or RNA. These may also be used to create transgenic plants in which the polypeptides a
                                                                                                                                                                                                                                                                                                                                                                                                                                      Nucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            overexpressed or suppressed, and as probes situ hybridisation (FISH).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             their enzyme activities. The polynucleotides are used as probes for genetically and physically mapping genes that they compose, and as markers for traits linked to those genes, where such information may be used in plant breeding to develop lines with desired phenotypes. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         deaminase and adenosine deaminase may be used to prepare antibodies to these proteins, and to design or identify herbicides that inhibit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               inosine. Mutations in these genes catabolism of adenosine and AMP. 1
                                                                                                                                                         Caspar T,
                                                                                                                                                                                                                   30-JUL-1999;
                                                                                                                                                                                                                                           28-JUL-2000; 2000WO-US21009
                                                                                                                                                                                                                                                                                         WO200109305-A2
                                                                                                                                                                                                                                                                                                                                                                           Glycine max.
                                                                                                                                                                                                                                                                                                                                                                                                              AMP deaminase;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAF25498;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAF25498 standard; DNA; 1447
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 530 BP; 156 A; 123 C; 98 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    white blood cells, which causes severe immunodeficiencies.
                                                                                                                       P-PSDB;
                                                                                                                                  WPI; 2001-159866/16.
                                                                                                                                                                              (DUPO ) DU PONT DE NEMOURS (PION-) PIONEER HI-BRED INT
                                                                                                                                                                                                                                                                                                                                                                                                   inosine;
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16; Conserv
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Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                adenosine deaminase; adenosine; transgenic plant;
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                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers 188..1255
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/product= "adenosine deaminase"
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                                                                                                                                                         Sakai H,
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                                                                                                                                                         Weng Z,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     150 T; 3 other;
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o death c
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RESULT 14
AAH41227/
ID AAH4
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Best Local S
Matches 16
The present invention relates to the genomic sequence of Pyrococcus abyssi and P. abyssi proteins (see ARB9603-ARB96842). P. abyssi is a hyperthermophilic archaeon, which is isolated from deep-sea hydrothermal vents. The present sequence is a fragment of the genomic sequence of P. abyssi. The 5' end of this sequence overlaps with the 3' end of AAH41226
                                                                                                                Claim
                                                                                                                                                 New nucleotide sequences isolated proteins useful in industry -
                                                                                                                                                                                                                                             Forterre P,
Querellou J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Key
                                                                                                                                                                                                        WPI; 2001-126236/14.
                                                                                                                                                                                                                                                                                                    (IFRE-)
                                                                                                                                                                                                                                                                                                                                                            21-APR-1999;
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Weissenbach
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                                                                                                                593-665;
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/note= "This sequence overlaps with the
AAH41226"
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J, Saurin
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Pred. No.
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                                                                                                                                                                    Pyrococcus
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2.8e+02;
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ABP43228) and to cDNAs encoding them (ABQ54131-ABQ56305), and also encompasses polypeptides 90% identical and polynucleotides 95% identical to the sequences of the invention. The invention additionally relates to recombinant vectors and host cells comprising human ovarian antigen polynucleotides, antibodies against human ovarian antigens, and the use of ovarian antigen polynucleotides and polypeptides in diagnosing, treating, prognosing or preventing various ovary and/or breast-related disorders. Such conditions include ovarian cancer and breast cancer, and

tumours of ovarian or

The invention relates to 2175 novel human ovarian antigens (ABP41054-ABP43228) and to cDNAs encoding them (ABQ54131-ABQ56305), and also

Claim 1; SEQ ID No 1467; 2922pp; English.

neurological diseases

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ABQ55587/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; ovarian antigen; ovary; ovarian; breast; cancer; tumour; ovarian cancer; breast cancer; tumour; reproductive system disord infertility; pregnancy disorder; anovulation; polycystic ovary sypcos; ovarian cyst; dysmenorrhoea; endocrine disorder; infection; inflammatory condition; immune disorder; blood disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         gene therapy; chromosome mapping;
antibody preparation; cytostatic;
antiinflammatory; gynaecological;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cardiovascular disorder; respiratory disorder; neurological disorder;
gastrointestinal disorder; urinary system disorder; drug screening;
gene therapy; chromosome mapping; forensic analysis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The proteins of the present invention have various potential industrial uses, since the proteins are stable at very high temperatures, some up to 110 degrees centigrade.

Note: This patent is in the same patent family as WO200065062, which
                                                                                                                                                                                     rsolated nucleic acid molecules encoding novel ovarian polypeptides, useful in the prevention, treatment and diagnosis of cancer (e.g. ovarian cancer), immune disorders, cardiovascular disorders and
                                                                                                                                                                                        ovarian cancer),
                                                                                                                                                                                                                                            WPI; 2002-147878/19
P-PSDB; ABP42510.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        antigen HODFV22 cDNA, SEQ ID NO:1467.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          reproductive; gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       immunomodulatory; neuroprotective;
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. 3.9e+02;
ches 0;
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Search completed: August 23, 2003, 10:38:17 Job time: 208.5 secs
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Best Local S
Matches 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    invention.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 611 BP; 212 A; 106 C; 120 G; 154 T; 19 other;
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                                                                                                                                                291 GTCAAATACCTTTGTGTCC 273
                                                                                                                                                                                           2 GTCAAAAACCGTTGTGTCC 20
                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                        79.0%; Score 15.8; DB 24; Length 611; 89.5%; Pred. No. 3.3e+02; Vative 0; Mismatches 2; Indels 0
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Maximum DB seq length: 2000000000
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Sequence:
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               14.8
14.8
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1: /cgn2_6/ptodata/2/

2: /cgn2_6/ptodata/2/

3: /cgn2_6/ptodata/2/
4: /cgn2_6/ptodata/2/
5: /cgn2_6/ptodata/2/
6: /cgn2_6/ptodata/2/
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Copyright (c) 1993 - 2003 Compu
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/cgn2_6/ptodata/2/ina/5B_COMB.seq:*
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US-08-461-038-9
US-08-461-645-9
US-08-000-094-19
US-09-000-094-21
US-09-000-094-23
US-09-000-994-23
US-09-000-996-5
US-09-345-236B-76
US-09-345-236B-80
US-09-345-236B-80
US-09-345-217-1
US-09-345-217-8
US-09-345-217-8
US-09-345-217-8
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US-09-345-217-8
US-09-345-217-8
US-09-128-155-16
US-09-345-217-8
US-08-487-283A-17
US-08-487-283A-21
US-08-487-283A-21
US-08-487-283A-21
US-08-487-283A-21
US-08-487-283A-11
US-08-487-283A-15
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Thes 20; Conserve
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US-08-479-817-9/c
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14.2	14.2	14.2	14.2	14.2	14.2	14.2	14.2	14.2	14.2	14.2	14.2	14.2	14.2	14.2	14.2	14.2	14.2
71.0	71.0	71.0	71.0	71.0	71.0	71.0	71.0	71.0	71.0	71.0	71.0	71.0	71.0	71.0	71.0	71.0	71.0
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US-09-292-034-1	US-08-874-162-1	US-08-485-241-1	US-08-299-675-1	US-09-195-966-1	PCT-US94-05277-1	US-09-041-886-24	US-09-972-800A-1	US-09-087-465-1	PCT-US95-17025-3	US-08-956-653A-3	US-09-364-970-10	US-08-948-547-3	US-08-956-869-3	US-08-956-652-3	US-08-820-754-3	US-08-852-091-3	US-08-369-796-3
Sequence 1, Appli	Sequence 24, Appl	Sequence 1, Appli	Sequence 1, Appli	Sequence 3, Appli	Sequence 3, Appli	Sequence 10, Appl	Sequence 3, Appli										

ALIGNMENTS

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CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/307,026
FILING DATE:
APPLICATION NUMBER: US 07/805,537
FILING DATE: 11-DEC-1991
ATTORNEY/AGENT INFORMATION:
NAME: EVANS, BAILY
REGISTRATION NUMBER: 22,802
REGISTRATION NUMBER: 370068-344(
TELEPHONE: (212) 840-3333
TELEFAX: (212) 840-0712
INFORMATION FOR SEQ ID NO: 9:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 9, Application US/08479817 Patent No. 5597910
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TOPOLOGY: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/479,817
FILING DATE:
                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 30 base pairs
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Gudibande, Satyanarayana
APPLICANT: Kenten, John H.
TITLE OF INVENTION: IMPROVED ELECTRO
TITLE OF INVENTION: FOR DNA PROBE AS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Curtis, Morris & Safford
ADDRESSEE: C/O Barry Evans
STREET: 530 Fifth Avenue
CITY: New York
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        USA
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Score 20; DB 1; Pred. No. 0.051; ; Mismatches

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GENERAL INFORMATION:
                                                                                                                                                                                  Sequence 9, Application Patent No. 5686244
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                                                                                                                                                                    GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 30 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: EVANS, BAITY
REGISTRATION NUMBER: 22,802
REFERENCE/DOCKET NUMBER: 37/
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Gudibande, Satyanarayana R. APPLICANT: Kenten, John H. TITLE OF INVENTION: IMPROVED ELECTROCH TITLE OF INVENTION: FOR DNA PROBE ASSA NUMBER OF SEQUENCES: 12

CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                TITLE OF INVENTION: IMPROVED ELECTROCHEMILIMINESCENT LABEL TITLE OF INVENTION: FOR DNA PROBE ASSAYS NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
                                                                                                                              APPLICANT: Gudibande, Satyanarayana R. APPLICANT: Kenten, John H.
                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/08/461,038 FILING DATE: 05-JUN-1995 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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STATE: New York
CITY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: nucleic acid
STRANDEDNESS: single
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                               ADDRESSEE:
                 STREET:
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 New York
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                   530 Fifth Avenue
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(212) 840-0712
R SEQ ID NO: 9:
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                               Curtis, Morris & Safford
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Pred. No. 0.051;
0; Mismatches
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US-09-000-094-19
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Best Local
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 30 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/08/
FILING DATE: 05-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: EVANS, BAITY
REGISTRATION NUMBER: 22,80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: 37
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 840-3333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
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             PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/AU96/00473
FILING DATE: 26-JUL-1996
APPLICATION NUMBER: AU PN 4439/95
FILING DATE: 27-JUL-1995
                                                                                                           CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/000,094
FILING DATE: 21-Apr-1998
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
ADDRESSEE: FOLEY & LARDNER
STREET: 3000 K Street, N.W
                                                                                                                                                                                                                                                                                                                                                                                                                  EDWARDS, Stirling John
TITLE OF INVENTION: PAPILLOMAVIRUS POLYPROTEIN CONSTRUCTS
NUMBER OF SEQUENCES: 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: WEBB, Elizabeth Ann
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DEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TGCTAATTCGGTGCTACCTG 10
                                                                                                                                                                                         COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                       COUNTRY: U.S.A. ZIP: 20007-5109
                                                                                                                                                                                                                                                                                                                            CITY: Washington STATE: D.C.
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IBM PC compatible
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MARGETTS, Mary Brigid COX, John Cooper
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                840-0712
INFORMATION
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US-09-000-094-21
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Patent No. 6365160
GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO: 21:
                                                                                                                       COUNTRY: U.S.A.

COUNTRY: U.S.A.

ZIP: 20007-5109

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION NUMBER: US/09/000,094

FILING DATE: 21-Apr-1998

CLASSIFICATION NUMBER: WO PCT/AU96/00473

PRIOR APPLICATION NUMBER: WO PCT/AU96/00473

APPLICATION NUMBER: WO PCT/AU96/00473

FILING DATE: 26-JUL-1996

APPLICATION NUMBER: WO PCT/AU96/00473

FILING DATE: 27-JUL-1995

ATTORREY/AGENT INFORMATION:

NAME: PRIOR STADNERS ATTORREY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local
         NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 017227/0137
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 672-5300
TELEFAX: (202) 672-5399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
ADDRESSEE: FOLEY & LARDNER
STREET: 3000 K Street, N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EDWARDS, Stirling John
TITLE OF INVENTION: PAPILLOMAVIRUS POLYPROTEIN CONSTRUCTS
NUMBER OF SEQUENCES: 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE DESCRIPTION: SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: DNA (genomic)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 1107 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: BENT, Stephen A.
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WILLIAMS, Mark Philip
MOLONEY, Margaret Bridget
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Pred. No.
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                                                                                                                       TELEFAX: (202) 6: INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                    COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/000,094
FILING DATE: 21-Apr-1998
CLASSIFICATION: CUNknown>
PRIOR APPLICATION NUMBER: WO PCT/AU96/00473
FILING DATE: 26-JUL-1996
APPLICATION NUMBER: AU PN 4439/95
FILING DATE: 27-JUL-1995
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
BERTENENET STEPHEN NUMBER: 29,768
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
es 20; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
ADDRESSEE: FOLEY & LARDNER
STREET: 3000 K Street, N.W
                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 1398 base pairs
                                                                                                                                                                                REFERENCE/DOCKET NUMBER: 017227/0137
TELECOMMUNICATION INFORMATION:
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EDWARDS, Stirling John
TITLE OF INVENTION: PAPILLOMAVIRUS POLYPROTEIN CONSTRUCTS
NUMBER OF SEQUENCES: 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 1128 base pairs
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SEQUENCE DESCRIPTION: SEQ ID NO:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear MOLECULE TYPE: DNA (genomic)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 TGCTAATTCGGTGCTACCTG 20
                                                   TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20007-5109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: Washington
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                                                                                                                                                                    TELEPHONE: (202) 672-5300
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                 TYPE: DNA (genomic)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MARGETTS, Mary Brigid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CDS
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Pred. No. 0.082;
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RESULT 7
US-09-000-094-45
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                                              US-09-000-094-45
Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 45, Application Patent No. 6365160
GENERAL INFORMATION:
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                                                                                                                                                                                                                   TELEFAX: (202) 672-5;
INFORMATION FOR SEQ ID NO: 45:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local 20;
                                                        LOCATION: 1..4761
SEQUENCE DESCRIPTION: SEQ
                                                                                                                                                                                                                                               TELEPHONE: (202) 672-5300
                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/000,094
FILING DATE: 21-Apr-1998
CLASSIFICATION: -CURROWN->
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
ADDRESSEE: FOLEY & LARDNER
STREET: 3000 K Street, N.W.
                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
                                                                                                         FEATURE:
                                                                                                                        MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT:
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                                                                                                                                                  LENGTH: 4770 base pairs TYPE: nucleic acid STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: WO PCT/AU96/00473 FILING DATE: 26-JUL-1996 APPLICATION NUMBER: AU PN 4439/95 FILING DATE: 27-JUL-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                           NAME/KEY:
                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: 01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: U.S.A. ZIP: 20007-5109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: Washington
                                                                                                                                                                                                                                                                                                            NAME: BENT, Stephen A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EDWARDS, Stirling John
OF INVENTION: PAPILLOMAVIRUS POLYPROTEIN CONSTRUCTS
R OF SEQUENCES: 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Application US/09000094
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COX, John Cooper
                                                                                                                                     linear
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 100.0%;
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Pred.
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No.
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 DB 4;
0.099;
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                                                                                                                                                      PCT-US95-11859-2
                                                                                                                                                                     RESULT 9
                                                                                                                      Sequence 2, Application PC/TUS9511859 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                             Query Match
Best Local
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                                                                                                                                                                                                                                                                               Matches
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APPLICATION NUMBER: US 08/310,468

FILING DATE: 22-SEP-1994

ATTORNEY/AGENT INFORMATION:

NAME: CARTY, CHRISTINE E.

NAME: CARTY OUNBER: 36,099

REGISTRATION NUMBER: 19307

TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: JANSEN, KATHRIN U.
APPLICANT: HOFMANN, KATHRYN J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE: (908) 594-6734
TELEFAX: (908) 594-4720
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                         APPLICANT: JANSEN, KATHRIN U. APPLICANT: HOFMANN, KATHRYN J. TITLE OF INVENTION: DNA ENCODING TITLE OF INVENTION: 6A
                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 8010 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-SOFTWARE: Patentin Release t CURRENT APPLICATION DATA:
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ADDRESSEE: CHRISTINE
                              NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: USA
ZIP: 07065-0900
                                                                                                                                                                                                                                                                                                                                                                                      STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER:
                ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2357 TGCTAATTCGGTGCTACCTG 2376
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                                                                                                                                                                                                                                                                                            Similarity
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CHRISTINE E. CARTY 6 E. LINCOLN AVENUE
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LINCOLN AVENUE -
                                                                                                                                                                                                                                                                            100.0%; So 100.0%; P ative 0;
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Pred. No. 0.
                                                                                                                                                                                                                                                                                 Mismatches
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   ı
                                                                             HUMAN PAPILLOMA VIRUS TYPE
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 P.O.
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BOX 2000
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RESULT 11
US-09-345-236B-76
; Sequence 76, Application US/09345236B
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US-09-228-986-5/c
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PCT-US95-11859-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 5, Application US/09228986 Patent No. 6359198
                                                                                                                                                              Matches
                                                                                                                                                                            Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                    SEQ ID NO 5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Strabala, Timothy
APPLICANT: Nieuwenhuizen, Niels
TITLE OF INVENTION: Compositions Isolated from Plant Cells
TITLE OF INVENTION: and Their Use in the modification of PJ
FILE REFERENCE: 11000/1020
                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/09/228,986
CURRENT: FILING DATE: 1999-01-12
                                                                                                                                                                                                                                                                                                               NUMBER OF SEQ ID NOS: 130
SOFTWARE: FastSEQ for Wind
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: (908) 594-4720
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                              LENGTH: 3340
TYPE: DNA
ORGANISM: Pinus radiata
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY:
ZIP: 07065-0907
COMPUTER READABLE FORM:
COMPUTER FLOPPY disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: CARTY, CHRISTINE E.
REGISTRATION NUMBER: 36,099
REFERENCE/DOCKET NUMBER: 19307 PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (908) 594-6734
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 0
FILING DATE: 22-SEP-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION DATA
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER:
                                                                                          1176 GCTAATTCGTTGCTACC 1160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      401 TGCTAATTCGGTGCTACCTG 420
                                                                                                           2 GCTAATTCGGTGCTACC 18
                                                                                                                                                              16;
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I Similarity 100.0%; Pred. No. 0.11;
20; Conservative 0; Mismatches
                                                                                                                                                             Conservative
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                                                                                                                                                                            77.0%;
94.1%;
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                                                                                                                                                         Score 15.4; D
Pred. No. 31;
0; Mismatches
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; NAME/KEY: CDS
; LOCATION: (13)...(165)
US-09-345-236B-78
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Best Local Similarity
Matches 16; Conserve
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; NAME/KEY: CDS
; LOCATION: (27)...(689)
US-09-345-236B-76
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CURRENT FILING DATE: 1999-06-30
NUMBER OF SEQ ID NOS: 148
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 78
LENGTH: 692
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: FastSEQ for Windows Version 3.0 SEQ ID NO 76
                                                            Matches
                                                                                        Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT:
                                                                                                                                                                                                                                                                                                 APPLICANT: Moser, Bettina
APPLICANT: Cockburn, Andrew
APPLICANT: White, Susan E.
APPLICANT: Undeen, Albert H.
TITLE OF INVENTION: Compositions, and Methods f
FILE REFERENCE: 21042.0004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/09/345,236B
CURRENT FILING DATE: 1999-06-30
NUMBER OF SEQ ID NOS: 148
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TITLE OF INVENTION: No. 6521454el Baculoviruses, I
TITLE OF INVENTION: Compositions, and Methods for
FILE REFERENCE: 21042.0004
                                                                                                                                                                                           TYPE: DNA
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                                                                                                                                                                           ORGANISM: mosquito baculovirus
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                                                                          Match 74.0%;
Local Similarity 88.9%;
165 CTAATTCGGCGCTGCCTG 182
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                                                                          Score 14.8;
Pred. No. 54;
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Pred. No. 5
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for Control of Invertebrates
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RESULT 13 US-09-345-236B-80/c ; Sequence 80, Application US/09345236B ; Patent No. 6521454

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; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(366)
; NAME/KEY: CDS
; LOCATION: (529)...(690)
US-09-345-236B-80
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APPLICANT: Undeen, Albert H.
TITLE OF INVENTION: No. 6521454el Baculoviruses, Insecticidal
TITLE OF INVENTION: Compositions, and Methods for Control of Invertebrates
FILE REFERENCE: 21042.004
CURRENT APPLICATION NUMBER: US/09/345,236B
CURRENT FILING DATE: 1999-06-30
NUMBER OF SEQ ID NOS: 148
SODTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 80
LENGTH: 692
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Best Local
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TYPE: DNA
ORGANISM: mosquito baculovirus
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642052
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APPLICATION NUMBER: 60/
FILING DATE: 1997-03-07
                                                            FILING DATE: 1997-05-23
APPLICATION NUMBER: 60/047,633
                                                                                                                           FILING DATE: 1997-0: APPLICATION NUMBER:
                                                                                                                                                                                                        APPLICATION NUMBER: 60/040,163 FILING DATE: 1997-03-07
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APPLICATION NUMBER: 60/040,336
                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: 60/040,626 FILING DATE: 1997-03-07
                APPLICATION NUMBER: 60/047,583 FILING DATE: 1997-05-23
                                                                                                            FILING DATE: 1997-05-23
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                                                                                                                                                                            FILING DATE: 1997-05-23
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                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: 60/040,333
                                               FILING DATE: 1997-05-
                                                                                            APPLICATION NUMBER: 60/047,502
                                                                                                                                                                                         APPLICATION NUMBER:
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88.9%;
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FILING DATE: 1997-08-6/0
APPLICATION NUMBER: 60/0
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                                                                                                                            FILING DATE: 1997-00 2-APPLICATION NUMBER: 60/08-22
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            FILING DATE: 1997-08-22
APPLICATION NUMBER: 60/056,909
FILING DATE: 1997-08-22
APPLICATION NUMBER: 60/056,875
FILING DATE: 1997-08-22
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APPLICATION NUMBER: 60/056,632
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APPLICATION NUMBER: 60/056,894
FILING DATE: 1997-08-22
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APPLICATION NUMBER: 60/056,876
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APPLICATION NUMBER: 60/043,670
                                                                                                                                                                                                                                           APPLICATION NUMBER: 60/047,501
                                                                                                                                                                                                                                                         FILING DATE: 1997-04-11
APPLICATION NUMBER: 60/043,576
FILING DATE: 1997-04-11
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FILING DATE: 1997-05-23
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APPLICATION NUMBER: 60/047,590
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FILING DATE: 1997-08-22
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FILING DATE: 1997-08-22
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FILING DATE: 1997-08-22
APPLICATION NUMBER: 60/056,880
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FILING DATE:
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; LENGTH: 11970
; TYPE: DNA
; ORGANISM: Homo sapiens
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APPLICANT: DUFF, GORDON W.
APPLICANT: COX, ANGELA
APPLICANT: CAMP, NICOLA J.
APPLICANT: CAMP, NICOLA J.
APPLICANT: DIGIOVINE, FRANCESCO S.
APPLICANT: INVENTION: DIGNOSTICS AND THERAPEUTICS FOR DISEASES ASSOCIATED
TITLE OF INVENTION: WITH AN IL-1 INFLAMMATORY HAPLOTYPE
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CURRENT APPLICATION NUMBER: US/09/345,217
CURRENT FILING DATE: 1999-06-30
EARLIER APPLICATION NUMBER: PCT/GB98/01481
EARLIER FILING DATE: 1998-05-21
EARLIER APPLICATION NUMBER: 9711040.7
EARLIER FILING DATE: 1997-05-29
NUMBER: 05-21
NUMBER: 05-29 ID NOS: 32
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ER FILING DATE: 1997-09-05
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 CC149256
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5 ZMMBBb15H
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KEYWORDS
SOURCE
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Contact: Rod Wing
Arizona Genomics Institute
University of Arizona
Biological Sciences West, 448A, P.
85721-0088, USA
Tel: 520 626 3967
Fax: 520 621 9288
Email: http://genome.arizona.edu
                                                                                                                                                                                                                                                                                                                                                                               Zea mays subsp. mays (maize)
Zea mays subsp. mays
Zea mays subsp. mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Eukaryota; Viridiplantae; Streptophyta; Enbryophyta; Poaceae; PACCAD
Spermatophyta; Magnollophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
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                                                                                                                Sequencing of the maize genome
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  PCR PRimers
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subsp. mays genomic
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                                                          Box 210088,
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CC134974 NDL.91K13
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BH878622 h883C03.b
B1114943 AU114943
BH397091 AG-ND-168
CC159313 1901C01.b
BF937261 ffm62g01.y
AQ678663 HS_2094_B
BQ378925 RC2-UT008
BJQ058697 AJ058697
CD437384 ELO1N0372
AQ766138 HS_479_B
BQ378925 RC2-UT008
BJQ058697 AJ058697
CD437384 ELO1N0372
AQ7491873 RPC1-11.y
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CC808529 CSU-K33r.
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Plate: 15 row:
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1 (bases 1 to 370)
Alcala,J., Vrebalov,J., White,R., van der Hoeven,R.S., Holt,I.E., Liang,F., Hansen,T.S., Craven,M.B., Bowman,C.L., Ronning,C.M., Nierman,W., Fraser,C.M., Martin,G.B., Giovannoni,J.J. and Tanksley
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Class: BAC ends.
                                                                                                                                                                                                                                                                                                                                                                                                                 Unpublished Contact: CU
                                                                                                                                                                                                                                                                                                                                                         Clemson University
100 Jordan Hall, Clemson, SC
                                                                                                                                                                                                                                                                                                                                                                                              Clemson University Genomics Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Generation of ESTs from tomato fruit tissue, breaker stage
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/note="Vector: pBeloBAC11; Site_1: HindIII;
HindIII; Zea mays L. ssp. mays"
145 c 178 g 286 t 1 others
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                                                 /note="Vector: pBluescriptSKmCUadapt; Site_1: EcoR1; Site_2: XhoI; Fruit were harvested at the breaker stage (first sign of lycopene accumulation on the blossom end the fruit). Fruit were cut in half and the seeds and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /mol_type="genomic DNA"
/cultivar="B73"
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/lab_host="DH10B"
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                                                                                                                                         /lab_host="SOLR"
                                                                                                                                                                                                                                  /mol_type="mRNA"
/cultivar="TA496"
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                                                                                                                           /clone_lib="tomato breaker fruit, TIGR"
                                                                                                                                                            /tissue_type="Pericarp"
/dev_stage="breaker"
                                                                                                                                                                                               /db_xref="taxon:4081"
/clone="cLEG33L22"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Mahairas GG, Wallace JC,
High Throughput Sequencing Center
University of Washington
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Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T., Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. a
                                                          Tetraodon nigroviridis genome surve
109D19 of library G from Tetraodon
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E-Coli DH10B"
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/mol_type-"genomic DNA"
/mol_type-"genomic DNA"
/db_xref="taxon:9606"
/clone="plate=2252 Col=12 Row-C"
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Submitted (12-APR-2000) Genoscope - Centre National of Submitted (12-APR-2000) Genoscope - Centre National of Submitted (12-APR-2000) Genoscope - FRANCE (E-mail : seqref@genome : www.genoscope.cns.fr)

This sequence is a single read and was generated as scale clone-end sequencing project of the Tetradon genome. For more information, please take a look at http://www.genoscope.cns.fr/Tetraodon.

Location/Qualifiers
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MDL.46E23.SP6 Notre Dame Liverpool

NDL.46E23, genomic survey sequence.
CC122092
CC122092.1 GI:29991147
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Characterization and repeat analysis of the compact genome of the freshwater pufferfish Tetraodon nigroviridis
Genome Res. 10 (7), 939-949 (2000)
                   Other_GSSs: NDL.46E23.T7
                                   Unpublished
                                                                                                                                        Aedes aegypti (yellow fever mosquito)
Aedes aegypti
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 Contact: Brendan Loftus
                                                Neoptera; Endopterygota; Diptera; Nematocera; Cu
1 (bases 1 to 600)
Loftus,B., Shetty,J., Knudson,D. and Severson,D.
BAC end sequencing of Aedes aegypti
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/mol_type-"genomic DNA"
/db_xref-"taxon:99883"
/clone-"109D19"
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Email: enta@tigr.org
Library was provided be
Seg primer: SP6
Class: BAC ends.
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Library was provided
Seg primer: SP6
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Tel: 301-838-3543
Fax: 301-838-0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Unpublished
Other_GSSs: NDL.91K13.T7
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Loftus, B., Shetty, J., Knudson, D. and Severson, D.
BAC end sequencing of Aedes aegypti
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Aedes aegypti (yellow fever mosquito)
Aedes aegypti
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Department of Eukaryotic Genomics
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/clone="NDL.46E23"
/clone=lib-"Notre Dame Liverpool"
/clone_lib-"Notre Dame Liverpool"
/note="Vector: pBCBACL; Site_1: Hind II; The library
prepared from whole body tissue of newly hatched Ll
by David Severson at the University of Notre Dame ar
Hongbin Zhang"
a 160 c 181 g 79 t
/Clone="NDL.91K13"
/Clone_lib="Notre Dame Liverpool"
/Clone_lib="Notre Dame Liverpool"
/note="Vector: pECBAC1; Site_l: Hind III; The library was prepared from whole body tissue of newly hatched L1 larvae by David Severson at the University of Notre Dame and Hongbin Zhang"
1 208 c 240 g 167 t
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/strain="Liverpool"
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/mol_type-"genomic DNA"
/strain-"Liverpool"
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/mol_type="genomic DNA"
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Pred. No. 1.1e+03;
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                                         BB570973 RIKEN full-length enriched, 0 day neonat musculus cDNA clone 4633401D12 5', mRNA sequence. BB570973 .1 GI:11461881 EST.
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                            Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Library was provided by David Seq primer: SP6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: enta@tigr.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Department of Eukaryotic Genomics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Brendan Loftus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Loftus, B., Shetty, J., Knudson, D. and BAC end sequencing of Aedes aegypti
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota,
Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Aec
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               musculus
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/note="Vector: pECBAC1; Site_1: Hind III; The library was
prepared from whole body tissue of newly hatched L1 larvae
by David Severson at the University of Notre Dame and
                                                                                                                                                                                                                                                                                                                          Hongbin Zhang"
1 221 c 2
                                                                                                                                                                                                                                                                                                                                                                                                            /mol_type="genomic DNA"
/strain="Liverpool"
/db_xref="taxon:7159"
/clone="NDL_91B22"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Aedes aegypti"
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Metazoa; Chordata; Craniata; Vertebrata;
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Euteleostomi;
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Query Match Best Local S Matches

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1 (bases 1 to 226)

Aizawa, K., Akahira, S., Akimura, T., Arai, A., Arakawa, T., Carninci, P.,

Aizawa, K., Akahira, S., Akimura, T., Hirozane, T., Hodoyama, Y.,

Imotani, K., Ishii, Y., Itoh; M., Izawa, M., Kawai, J., Kojima, Y., Konno,

H., Kusakabe, M., Matsuyama, T., Miyazaki, A., Nakamura, M., Nishi, K.,

Nomura, K., Numazaki, R., Okazaki, Y., Okido, T., Owa, C., Sakai, C.,

Komura, K., Numazaki, R., Okazaki, Y., Shibata, Y., Shinagawa, A.,

Sakai, K., Sasaki, D., Sato, K., Shibata, K., Shibata, Y., Shinagawa, A.,

Shiraki, T., Sogabe, Y., Suzuki, H., Tagawa, A., Takahashi, F., Tanaka

T., Toya, T., Watahiki, A., Yamamura, T., Yasunishi, A., Yoshida, K.,

Yoshiki, A., Muramatau, M. and Hayashizaki, Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Carninci, P., Nishiyama, I., wescover, N., Okazaki, Y., Nuramatsu, M. and Hayashizaki, Y.

N., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.

Thermostabilization and thermoactivation of thermolabile enzymes by trehalose and its application for the synthesis of full length cDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998)

Itoh, M., Kitsunai, T., Akiyama, J., Shibata, K., Izawa, M., Kawai, J.,

Tomaru, Y., Carninci, P., Shibata, Y., Ozawa, Y., Muramatsu, M., Okazaki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: genome-res@gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp/
Carninci.P., Nishiyama.Y., Westove
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ,Y. and Hayashizaki,Y.

Automated filtration-based high-throughput plasmid preparation system. Genome Res. 9 (5), 463-470 (1999)

Carninci,P. and Hayashizaki,Y.
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The Institute of Physical and Chemical Research (RIKEN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1-7-22 Suehiro-cho, Tsurumi-ku,
Tel: 81-45-503-9222
Fax: 81-45-503-9216
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                     contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5' GAGAGAGAAGGAICCAACAGCTCTTTTTTTTTTTTTTTTVN 3'], cDNA was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     prepared and sequenced in Mouse Genome Encyclopedia
Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory
                                                                                                                                                                                                                                                                                                                                                    prepared by using trehalose thermo-activated reverse
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/mol_type="mRNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /tissue_type="skin"
/dev_stage="0 day neonate"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /strain="C57BL/6J"
/db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="Site_1: SalI; Site_2: BamHI; cDNA library was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone_lib="RIKEN full-length enriched, 0 day neonate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /sex="mixed"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone="4633401D12"
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TGCTAATTCGGTGCTACCT

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RESULT 9
BH878622/c
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AU114943/c
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                                                                                                                                                                                                             44
                                   300 bp mRNA linear EST 19-OC: AUI14943 unpublished oligo-capped cDNA library Caenorhabditis elegans cDNA clone yk723hl 3', mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Lita Annenberg Hazen Genome Sequencing Center Cold Spring Harbor Laboratory PO Box 100, Cold Spring Harbor, NY 11724, USA Tel: 516 367 8884

Fax: 516 367 8874
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.
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hs83c03.b1 WGS-ZmaysF (JM107 adapted methyl filtered) Zea mays
genomic clone hs83c03 5', genomic survey sequence.
                                                                                                                                                                                                                                                       2 GCTAATTCGGTGCTACCTG 20
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Seq primer: -21Ml3UnivFwd
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Contact: W. Richard McCombie
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                    AU114943.1 GI:10928510
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: mccombie@cshl.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Genomic shotgun sequences from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 (bases 1 to 273)
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                          78
                                                                                                                                                                                                                                                                                                                                                                                                 /Clone_lib="WGS_ZmaysF (JM107 adapted methyl filtered)"
/note="Organ: immature ears; Site_1: Xba I; Site_2: Xba I;
The vector was digested with XbaI and one nucleotide was added by fill in in the recessive 3' end. The genomic DNA was nebulized, end repaired, adaptor ligated and size fractionated using sephadex. The resulting fragments were between 0.8 and 3 kb and were cloned into the vector (.x/y reads in M13mp19, .b/g reads in pUC19). The same ligation was transformed in either JM107 or DH5a. "

58 c 47 g 90 t
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/clone="hs83c03"
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/cultivar="B73"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /lab_host="JM107 or DH5a"
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                                                                                                                                                                                                                                                                                                                 79.0%;
89.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BH397091 376 bp DNA linear
AG-ND-168H24.TF ND-TAM Anopheles gambiae genomic
, genomic survey sequence.
BH397091
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Caenorhabditis elegans
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;
Rhabditidae; Peloderinae; Caenorhabditis.

1 (bases 1 to 300)
                                                                      Contact: Brendan J Loftus
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville,
Tel: 301 838 0208
Fax: 301 838 3543
                                                                                                                                                                                                                                                                                                                                                                                                 Anopheles gambiae
Anopheles gambiae
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
This clone is from an A. gambiae BAC library (ND-TAM) provided by F.H. Collins and sequenced by The Institute for Genomic Research (TIGR). The BAC library was generated from A. gambiae PEST strain
                                                                                                                                                                                                                                       Construction of a BAC library and generation of BAC sequence-tayged connectors for genome sequencing of malaria mosquito Anopheles gambiae Mol. Genet. Genomics 268 (6), 720-728 (2003)
                                                                                                                                                                                                                                                                                                                              Hong,Y.S., Hogan,J.R., Wang,X., Sarkar,A., Sim,C., Loftus,B.J.,
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National Institute of Genetics
Yata 1111, Mishima, Shizuoka 4
                                                                                                                                                                                      Other_GSSs: AG-ND-168H24.TR
                                                                                                                                                                                                                                                                                                                 and Collins, F.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BH397091.1 GI:17343307
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     and Sugano, S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Kohara, Y., Shin-1, T., Thierry-Mieg, J., Thierry-Mieg, D., Suzuki, Y.
                                                                                                                                                                                                       12655398
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Anopheles gambiae (African malaria mosquito)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: ykohara@lab.nig.ac.jp.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                    (bases 1 to 376)
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                                                     bjloftus@tigr.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Caenorhabditis elegans"
/mol_type="mRNA"
/strain="N2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone_lib="unpublished oligo-capped cDNA library" 62 \text{ c} \qquad 46 \text{ g} \qquad 97 \text{ t}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /sex="Hermaphrodite"
/tissue_type="whole animal"
/dev_stage="varied"
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/clone="yk723h1"
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one AG-ND-168H24
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Matches 17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Zea mays
Zea mays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          400 bp
1901c01.b1 WGS-ZmaysF (DH5a methyl
1901c01, genomic survey sequence.
CC159313
CC159313.1 GI:30184091
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                                                                                                                                                                                                                                                                                                                                                                               Email: mccombie@cshl.org
Plate: 1g01 row: c column:
                                                                                                                                                                                                                                                                                                                                                                                                                             Tel: 516 367 8884
Fax: 516 367 8874
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Lita Annenberg Hazen Genome Sequencing Center Cold Spring Harbor Laboratory PO Box 100, Cold Spring Harbor, NY 11724, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rabinowicz, P.D., O'Shaughnessy, A.L., Balija, V., Katzenburger, F., King, L., Miller, B., Muller, S., Zutavern, T., McCombie, W.R. and Martienssen, R.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Seq primer: M13 For Class: BAC ends.
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Location/Qualifiers
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Seq primer: -21M13UnivFwd
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Lita Annenberg Hazen Genome &
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17; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /mol_type="genomic DNA"
/strain="PEST"
/db_xref="taxon:7165"
/clone="AG-ND-168H24"
/clone_lib="ND-TAM"
/note="Vector: pECBAC1; S
a 75 c 101 g 92
/clone_lib="WGS-ZmaysF (DH5a methyl filtered)"
/note="Organ: immature ears; Site_1: Xba I; Site_2: Xba I;
/note="Torgan: immature ears; Site_1: Xba I; Site_2: Xba I;
The vector was dijested with XbaI and one nucleotide was added by fill in in the recessive 3' end. The genomic DNA was nebulized, end repaired, adaptor ligated and size fractionated using sephadex. The resulting fragments were
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism-"Anopheles gambiae"
/mol_type-"genomic DNA"
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                                                                                                                                          /lab_host="DH5a"
                                                                                                                                                                                   /db_xref="taxon:4577"
                                                                                                                                                                                                            /mol_type="genomic DNA"
/cultivar="B73"
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                                                                                                                                                                   /clone="ig01c01"
                                                                                                                                                                                                                                                       /organism="Zea mays"
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Pred. No. 1.8e+03;
0; Mismatches 2
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Zea mays (methyl
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filtered) Zea mays
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RESULT 13
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                                                                          Query Match
Best Local S
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Best Local :
                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                (web address: www.rzpd.de)
Seq primer: T3 ET from Amersham
Seq primer: T4 ecquence stop: 421.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Clark,M., Johnson,S.L., Lehrach,H., Lee,R., Li,F., Marra,M., J., S., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylle,T., Undd., K., Steptoe,M., Theising,B., Allen,M., Bowers,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R., Ritter, Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R., Waterstoned
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BF937261 427 bp mRNA linear EST 13-FEI fm62g01.yl Zebrafish adult retina cDNA Danio rerio cDNA clone mAGE:4200001 5', mRNA sequence.
                     N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: zbrafishewatson.wustl.edu
Library constructed by: Chandra Tucker and Gregory Niemi DNA
Sequencing by: Washington University Genome Sequencing Centes
distribution: RessourcenZentrumPrimarDatenbank, Berlin, Germa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Stephen L. Johnson
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eu
Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
; Cyprinidae; Danio.
1 (bases 1 to 427)
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GCTAATTCGGTGCTACCTG
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                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Zebrafish EST Project 1998
                                                                                                                                        /dev_stage="1-2 years"
/lab_host="E.Coli XL1-Blue MRF' (XL1-Blue MRF')."
/clone_lib="Zebrafish adult retina CDNA"
/clone_lib="Zebrafish adult retina CDNA"
/note="Yector: Lambda ZAP II (pBluescript SK-); /
ECORI; Site_2: SalI; This Zebrafish library was
constructed by Dr. Susan E. Brockerhoff (email:
sbrocker@u.washington.edu) RZPD library number:
a 106 c 97 g 89 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   between 0.8 and 3 kb and were cloned into the vector (.x/y reads in M13mp19, .b/g reads in pUC19). The same ligation was transformed into DH5a."

73 c 72 g 127 t
                                                                                                                                                                                                                                                                                                                     /strain="wild-type"
/db_xref="taxon:7955"
/clone="IMAGE:4200001"
                                                                                                                                                                                                                                                                                                                                                                         /organism="Danio rerio"
/mol_type="mRNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                                                                      /sex="mixed"
                                                                          79.0%;
89.5%;
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Pred. No. 1.9e+03;
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                                                                          Score 15.8;
Pred. No. 1.
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Waterston, R.
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GCTAATTCAGTGCTAGCTG

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RESULT 15
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LOCUS
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VERSION
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Best Local :
   AUTHORS
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RC2-UT0087-200900-110-h04
BQ378925
BQ378925.1 GI:21054439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 TGCTAATTCGGTGCTACCT 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Clones may be purchased from Research Genetics (info@resgen.com). BAC end Web Server: http://www.htsc.washington.edu Plate: 2094 row: L column: 20 Seq primer: M13 Reverse Class: BAC ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        High Throughput Sequencing Center University of Washington
401 Queen Anne Avenue North, Seat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AQ678663 470 bp DNA HS_2094_B2_F10_MR CIT Approved Human Gen sapiens genomic clone Plate=2094 Col=20
                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 523)
                                                                                                                          Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     High quality sequence stop: 470.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Mahairas GG, Wallace JC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence-tagged connectors: A sequence approach to mapping and scanning the human genome Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
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1 (bases 1 to 470)

Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T., Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Adams,M.D. and Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Adams,M.D. and Mahairas,G.G., Wallace,J.C., Furlong,J., Young,J., Zhao,S., Adams,M.D. and Mahairas,G.G., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and Mahairas,G.G., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and Mahairas,G.G., Wallace,G.C., Smith,K., Swartzell,S., Adams,M.D. and Mahairas,G.G., Wallace,G.C., Smith,K., Swartzell,S., Adams,M.D. and Mahairas,G.G., Wallace,G.C., Wallace,G.C.,
                                                                                                                                                        Homo sapiens (human)
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(206) 616-3887
l: jwallace@u.washington.edu
Neto, E., Garcia Correa, R., Verjovski-Almeida, S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
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/note="Organ: Sperm; Vector: pBeloBAC11; BAC
B-Coli DH10B"
1 100 c 79 q 168 +
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Email: asimpsoneludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
This sequence was derived from the following URL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=RC26t2=RC2-UT0087-200900-110-h046t3=2000-09-206t4=1)
Seq_primer: puc 18 forward
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Ludwig Institute for Cancer Research
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//note="Organ: uterus_tumor; Vector: pucl8; Site_1: SmaI;
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Site_2: SmaI; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."
109 c 99 g 152 t
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/mol_type="mRNA"
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/cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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457	457 457	245	3340	14469	287	287	287	287	281	281	281	281	427	Query Match Length
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US-10-027-632-298306	US-10-027-632-35375	US-10-044-090-752	US-10-101-464A-5	US-10-128-/14-25/	US-10-074-095-170	US-10-079-854-36	US-09-764-860-170	US-09-764-878-36	US-10-074-095-928	US-10-079-854-249	US-09-764-860-928	US-09-764-878-249	US-10-027-632-74539	ID
	Sequence 35375, A	Sequence 752, App	sequence is, Appli	Sequence 257, App	Sequence 170, App	Sequence 36, Appl	Sequence 170, App	Sequence 36, Appl	Sequence 928, App	v		Sequence 249, App	Sequence 74539, A	Description

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72.0 72.0 71.0	72.0 72.0 72.0	74.0 74.0 74.0 74.0 72.0		76.0 76.0 76.0 75.0 74.0 74.0 74.0
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13 9	13 13 13	113 114 115	14 13 11 13	13 13 13 13 13 13 13 13 13 13 13 13 13 1
US-10-027-632-252550 US-09-965-703-60 US-09-813-358-49	US-10-027-632-202394 US-10-027-632-160032 US-10-027-632-160033 US-10-027-632-160033 US-10-027-632-252549	US-09-845-129-1 US-10-172-919-1 US-10-167-127-1 US-09-764-872-717 US-10-095-407-16 US-09-848-616-83	US-10-027-632-216899 US-09-809-391-80 US-10-027-632-264047 US-10-108-605-316 US-10-178-782-3	US-10-027-632-198643 US-10-027-632-198644 US-10-027-632-155367 US-10-027-632-262303 US-09-918-995-12873 US-09-027-632-243504 US-10-027-632-27924 US-10-027-632-27925 US-10-027-632-27926
Sequence 252550, Sequence 60, Appl Sequence 49, Appl	Sequence 202395, Sequence 202395, Sequence 160032, Sequence 160033, Sequence 252549,			Sequence 198643 Sequence 198644 Sequence 163367 Sequence 262303 Sequence 12873, Sequence 243504 Sequence 27924, Sequence 27925, Sequence 27926,

## ALIGNMENTS

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; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: FastSEQ for W
; SEQ ID NO 74539
; LENGTH: 427
; LENGTH: 427
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-74539
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, Sequence 74539, Application US/10027632
; GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
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                                                                           Query Match
Best Local Similarity
Matches 17; Conserv
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PRIOR FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR FILING DATE: 2000-02-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION NUMBER: US/10/027,632 CURRENT FILING DATE: 2002-04-30
                                                                                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: US 60/146,002 PRIOR FILING DATE: 1999-08-09
                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: US 60/156,358 PRIOR FILING DATE: 1999-09-28
                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: US 60/167,363 PRIOR FILING DATE: 1999-11-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR FILING DATE: 2000-04-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: US 60/218,006 PRIOR FILING DATE: 2000-07-12
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Conservative
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                                                                                               Score 17;
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; TYPE: DNA; ORGANISM: Homo sapiens US-09-764-878-249
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; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-860-928
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GENERAL INFORMATION:
APPLICANT: ROSen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PA121
SEQ ID NO
LENGTH:
                                                                               Sequence 249, Application US/10079854
Publication No. US20030054368A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PA121C1
CURRENT APPLICATION NUMBER: US/10/079,854
CURRENT FILING DATE: 2002-02-22
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APPLICANT: Rosen et al.
TITLE OF INVENTION: Nuc
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SEQ ID NO 249
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CURRENT FILING DATE: 2001-01-17
                                                Prior Application removed - See File Wrapper or Palm NUMBER OF SEQ ID NOS: 428
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FH: 281
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CURRENT FILING DATE: 2002-02-14
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TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
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PRIOR FILLING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: 60/214,886
PRIOR FILING DATE: 2000-06-28
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DR APPLICATION NUMBER: 60/225,267
DR FILING DATE: 2000-08-14
DR APPLICATION NUMBER: 60/216,880
DR FILING DATE: 2000-07-07
DR APPLICATION NUMBER: 60/225,270
DR FILING DATE: 2000-08-14
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FILLIG DATE: 2000-07-11
APPLICATION NUMBER: 60/225,447
FILING DATE: 2000-08-14
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APPLICATION NUMBER: 60
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FILING DATE: 2000-09-
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FILING DATE: 2000-09-
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FILING DATE: 2000-12-08
APPLICATION NUMBER: 60/235,834
FILING DATE: 2000-09-27
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DR APPLICATION NUMBER: 60/229,343
DR FILLING DATE: 2000-09-01
DR APPLICATION NUMBER: 60/229,345
DR FILLING DATE: 2000-09-01
DR FILLING DATE: 2000-09-01
DR APPLICATION NUMBER: 60/229,287
DR FILLING DATE: 2000-09-05
DR APPLICATION NUMBER: 60/229,513
DR FILLING DATE: 2000-09-05
DR APPLICATION NUMBER: 60/231,413
DR FILLING DATE: 2000-09-08
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DR APPLICATION NUMBER: 60/236,367
DR APPLICATION NUMBER: 60/236,367
DR APPLICATION NUMBER: 60/237,038
DR APPLICATION NUMBER: 60/236,370

APPLICATION NUMBER: 60/237,037
ETILING DATE: 2000-10-02
APPLICATION NUMBER: 60/237,040

FILING DATE: 2000-09-29
APPLICATION NUMBER: 60/236,802
FILING DATE: 2000-10-02

OR APPLICATION NUMBER: 60/225,268
OR FILING DATE: 2000-08-14
OR FILING DATE: 2000-09-29
OR APPLICATION NUMBER: 60/251,856
OR FILING DATE: 2000-12-08
OR APPLICATION NUMBER: 60/229,344

APPLICATION NUMBER: 60/: FILING DATE: 2000-09-01 APPLICATION NUMBER: 60/: FILING DATE: 2000-09-25

60/234,997

FILING DATE: 2000-09-29
APPLICATION NUMBER: 60/241,785
FILING DATE: 2000-10-20
APPLICATION NUMBER: 60/244,617
FILING DATE: 2000-11-01

FILING DATE: 2000-10-20
APPLICATION NUMBER: 60/249,299
FILING DATE: 2000-11-17
APPLICATION NUMBER: 60/236,327

NUMBER: 60/241,809

Query Match Best Local S Matches 17 17; Conservative 79.0%; 89.5%; Score 15.8; DB 14; Pred. No. 1e+02; 0; Mismatches 2; Length Indels 281; 0 Gaps

DR FILING DATE: 2000-10-02

OR APPLICATION NUMBER: 60/240,960

RE FILING DATE: 2000-10-20

OR APPLICATION NUMBER: 60/239,935

OR APPLICATION NUMBER: 60/239,935

OR APPLICATION NUMBER: 60/241,787

OR APPLICATION NUMBER: 60/241,787

OR APPLICATION NUMBER: 60/246,474

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OR APPLICATION NUMBER: 60/226,681

OR APPLICATION NUMBER: 60/225,759

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OR APPLICATION NUMBER: 60/225,213

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Patent No. US20020094953A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and
                                                                                                                                                                                                                                                             SOFTWARE: PatentIn Ver.
SEQ ID NO 170
LENGTH: 287
TYPE: DNA
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 Sequence
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TITLE OF INVENTION: Nucleic Acids, Proteins,
FILE REFERENCE: PA121
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CURRENT FILING DATE: 2001-01-17
                                                                                                                                                                                                       FEATURE:
NAME/KEY: SITE
LOCATION: (1)
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LOCATION: (1)
OTHER INFORMATION: n equals a,t,g,
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; OTHER INFORMATION: n equals a,t,g, or
US-10-079-854-36
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Matches 17
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APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PA121C1
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CURRENT FILING DATE: 2002-02-22
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NAME/KEY: misc_feature
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TYPE: DNA
ORGANISM: Homo sapiens
                                                                 APPLICATION NUMBER: 60/
FILING DATE: 2000-08-14
                                                                                                      APPLICATION NUMBER: 60/216,647 FILING DATE: 2000-07-07
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                APPLICATION NUMBER: 60/225,270
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b. US20030077704A1
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N NUMBER: 60/31, 414  E: 2000-09-08  N NUMBER: 60/231, 244  N NUMBER: 60/233, 064  E: 2000-09-14  R: 2000-09-14	: 2000-11-17 : 2000-10-11-17 : 2000-11-17 : 2	NUMBER: 60/249, 21 NUMBER: 60/215, 13 NUMBER: 60/215, 13 NUMBER: 60/225, 26 NUMBER: 60/249, 21 NUMBER: 60/249, 21 NUMBER: 60/249, 20 NUMBER: 60/249, 21 NUMBER: 60/249, 20 NUMBER: 60/249, 24 NUMBER: 60/249, 24	2000-11-08 2000-11-08 2000-11-09 NUMBER: 60/249, 21 2000-11-17 2000-11-17 2000-11-17 2000-11-17 2000-08-12 2000-08-14 2000-08-14 2000-08-14 2000-08-14 2000-08-14 2000-08-14 2000-08-14 2000-08-14 2000-08-14 2000-08-14 2000-08-14 2000-08-14 2000-08-15 2000-08-15 2000-08-16 2000-08-17 2000-08-18 2000-08-18 2000-08-18 2000-08-18 2000-08-18 2000-08-18
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DR APPLICATION NUMBER: 60/235, 834

PRILING DATE: 2000-09-27

PREPLICATION NUMBER: 60/234, 274

PREPLICATION NUMBER: 60/234, 274

PREPLICATION NUMBER: 60/224, 518

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PREPLICATION NUMBER: 60/236, 369

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PREPLICATION NUMBER: 60/236, 369

PREPLICATION NUMBER: 60/225, 268

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PREPLICATION NUMBER: 60/225, 268

PREPLICATION NUMBER: 60/229, 344

PREPLICATION NUMBER: 60/229, 345

PREPLICATION NUMBER: 60/231, 413

PREPLICATION NUMBER: 60/237, 039

PREPLICATION NUMBER: 60/239, 935

PREPLICATION NUMBER: 60/239, 935

PREPLICATION

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RESULT 11
US-10-295-362-19/c
US-10-295-362-19/c
; Sequence 19, Application US/10295362
; Publication No. US20030143745A1
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US-10-128-714-257/c
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Matches 17
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APPLICANT: Hu, Wei
APPLICANT: Tishko:
APPLICANT: Zamudi
APPLICANT: Eroshk
APPLICANT: Lemieu:
                                                       GENERAL INFORMATION:
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APPLICANT: Lemieux, Sebastien M
TITLE OF INVENTION: Identification of Essential Genes in Aspergillus fumigatus (
TITLE OF INVENTION: Methods of Use
FILE REFERENCE: 10182-018-999
CURRENT APPLICATION NUMBER: US/10/128,714
CURRENT ELLING DATE: 2002-04-23
PRIOR APPLICATION NUMBER: US 60/285,697
PRIOR PILING DATE: 2001-04-23
PRIOR APPLICATION NUMBER: US 60/287,066
PRIOR FILING DATE: 2001-04-27
PRIOR FILING DATE: 2001-06-05
PRIOR APPLICATION NUMBER: US 60/295,890
PRIOR FILING DATE: 2001-06-05
PRIOR FILING DATE: 2001-06-05
PRIOR FILING DATE: 2001-06-05
APPLICANT: Aventis Pharma
APPLICANT: Martinez, Asur
APPLICANT: Kolvek, Stever
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PRIOR FILING DATE: 2001-07-09
PRIOR APPLICATION NUMBER: US 60/316,362
PRIOR FILING DATE: 2001-08-31
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FILING DATE: 2000-10-20
APPLICATION NUMBER: 60/241,826
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Tishkoff, Daniel
Zamudio, Carlos
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US-10-044-090-752; Sequence 752, Application No. US20; GENERAL INFORMATION:
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Matches
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SOFTWARE: FastSEQ for
SEQ ID NO 5
LENGTH: 3340
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SEQ ID NO 19
LENGTH: 14468
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Best Local (
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APPLICANT: Nieuwenhuizen, Nicolaas
APPLICANT: Higgins, Colleen M.
TITLE OF INVENTION: Compositions Isolated from Plant Cells
TITLE OF INVENTION: and Their Use in the Modification of Plant Cell Signaling
FILE REFERENCE: 11000.1020c2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: Expressing and Assay FILE REFERENCE: USAVZ2001/0145 PCT CURRENT APPLICATION NUMBER: US/10/295,362 CURRENT FILING DATE: 2002-11-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: 60/162,866
PRIOR FILING DATE: 1999-11-01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION NUMBER: 09/704,302
PRIOR FILTNG DATE: 2000-11-01
PRIOR APPLICATION NUMBER: 09/228,986
PRIOR FILING DATE: 1999-01-12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: Genetically Modified Bacterial Strains and No. US20030143745A1
TITLE OF INVENTION: Expressing and Assaying Natural Products
APPLICANT: Olga Bandman
TITLE OF INVENTION: GENES DIFFERENTIALLY EXPRESSED IN VASCULAR TISSUE ACTIVATION
FILE REFERENCE: PA-0028 US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/10/101,464A
CURRENT FILING DATE: 2002-03-18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION NUMBER: PCT/US00/00724
                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA
ORGANISM: Pinus radiata
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16; Conserv
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                                                                           Application US/10044090
o. US20020137081A1
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Pred. No. 1
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Pred. No. 2.
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CURRENT

NUMBER: US/10/044,090

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; SEQ ID NO 35375; LENGTH: 457; TYPE: DNA; ORGANISM: Human US-10-027-632-35375
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US-10-027-632-35375/c
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; OTHER INFORMATION: Incyte ID No. US20020137081A1 034851.1
US-10-044-090-752
Sequence 60413, Application US/10027632
Sequence 60413, Application US/10027632
GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; CURRENT FILING DATE: 2002-04-30
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Best Local S
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NUMBER OF SEQ ID NOS: 850
SOFTWARE: PERL Program
SEQ ID NO 752
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR FILING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR FILING DATE: 2000-03-29
PRIOR FILING DATE: 2000-03-29
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TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
FILE REFERENCE: 108827.129
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CURRENT FILING DATE: 2002-04-30
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TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
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RAPPLICATION NUMBER: US 60/146,002
FILING DATE: 1999-08-09
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FILING DATE: 1999-11-23
APPLICATION NUMBER: US 60/156,358
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Pred. No. 2.1e
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                                                               Query Match
Best Local Similarity
Matches 17; Conserv
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                                                                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER: US 60/156,358 PRIOR FILING DATE: 1999-09-28 PRIOR APPLICATION NUMBER: US 60/146,002 PRIOR FILING DATE: 1999-08-09
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PRIOR FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR FILING DATE: 1999-11-23
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PRIOR FILING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR FILING DATE: 2000-03-29
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR FILING DATE: 2000-07-12
                                                                                                                                                                                       TYPE: DNA
                                                                                                                                                                                                         ENGTH: 457
418 TGCTAATTCTCTGCTACATG 437
                                   1 TGCTAATTCGGTGCTACCTG 20
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Search completed: August 23, 2003, 13:53:17 Job time: 142 secs

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length: 2000000000
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1: gb_ba:
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score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

## Result No. Score Query Match 100.0 100.0 100.0 88888 238650 242958 245636 252185 290670 348250 165468 173316 231561 192687 198067 213001 214621 223389 466 667 168268 298050 147349 Length 1751 2065 2443 7916 28939 34216 34589 37482 DB AC112011 AC025871 AC122980 AC121043 AP003592 0 AL807796 AL935260 AC131316 BX530057 AC118630 AC118630 AC118630 AC118630 AC118630 AC118633 AF246444 BPC31ATTP BC044687 AB017002 HPU31784 AL391808 U57054 1 PAPA6B AR169144 AX301236 PPHE6E AF092932 HPU40822 AF436130 ARI6914 Sequence L41216 Human papil AF69293 Human papil AF692931 Uniman papil AF436130 Human papil AF131823 Mouse DNA AC112911 Rattus no AC112911 Rattus no AC122980 Rattus no AC121043 Rattus no AC121043 Rattus no AC121046 Rattus no AC121047 Rouse DNA AL935260 Lactobaci AP003592 Nostoc sp AL807796 Mouse DNA AL935260 Lactobaci AP005800 Oryza satt AC131316 Mus muscu BX530057 Danio rer AC118630 Mus muscu AC124524 Mus muscu AC124524 Mus muscu AC108412 Mus muscu AC108414 Ac1dithio X57036 Bacteriopha AX301236 Sequence E05232 Part of DNA E05256 Primer for I34500 Sequence 9 I73213 Sequence 9 AF156428 Human pap AR202651 Sequence AR202652 Sequence AR202651 Sequence AR202671 Sequence AR202671 Sequence AR20203 Genital hum U31784 Human papil AL391808 Human DNA U57054 Caenorhabdi BC044687 Xenopus 1 AB017002 Dugesia j AJ006589 Bacteriop AC112240 Homo sapi Description Caenorhab

## ALIGNMENTS

JOURNAL	TITLE	AUTHORS	REFERENCE		ORGANISM	SOURCE	KEYWORDS	VERSION	ACCESSION	DEFINITION	LOCUS	AX301236	RESULT 1
Patent: WO 0185994-A 5 15-NOV-2001; Bioanalisi Centro Sud S.N.C. Di Perseu Siniblado EC. (IT)	Method and means for identifying hpv virus	Perseu, S., de Montis, A. and Floris, M.M.	1	artificial sequences.	synthetic construct	synthetic construct	•	AX301236.1 GI:17382323	AX301236	Sequence 5 from Patent WO0185994.	AX301236 20 bp DNA linear PAT 30-NOV-2001		

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E05256
Primer for amplifying
E05256
E05256.1 GI:2173446
JP 1993192200-a/26.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              OS Artificial ge
OC Artificial ge
OC Artificial se
OS Human papillo
PN JP 1993192200
PD 03-AUG-1993 J
PF 19-AUG-1990 J
PR 20-AUG-1990 J
PR 20-AUG-1990 J
PR 20-AUG-1990 J
PR 70-AUG-1990 J
PR 70-
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Chazawa, K., Shimada, M., Katou, I., Fukushima, M.
DETECTION OF HUMAN PAPILLOMA VIRUS
PATENT: JP 1993192200-A 2 03-AUG-1993;
TAKARA SHUZO CO LTD
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                                                                                                                                                                                                                                                                         Similarity
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C12Q1/70,C12Q1/68;
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19-AUG-1991 JP 1991230839
20-AUG-1990 JP 90P 217067
0KAZAWA KAZUHIDE, SHIMADA MASAMITSU, KATOU IKUNOSHIN,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Artificial gene
Artificial sequence; Genes.
Human papillomavirus
JP 1993192200-A/2
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of DNA sequence of Human papillomavirus
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  topology: Linear;
hypothetical: No;
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/mol_type="genomic DNA"
/db_xref="taxon:32630"
/note="primer representative of region E6 of
HPV virus having low oncogenic hazard"
1 5 c 5 g 7 t
                                                                                                                                                                                                                                                                                                                                              /organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630" 7 t
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157335/c
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I34500/c
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PUKUSHIMA MICHIO,
PI FUJINAGA KEI
PC C1201/70, C120,
CC strandedness:
CC topology: Lin
CC hypothetical:
CC anti-sense: N
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I34500
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Gudibande, S.R. and Kenten, J.H.
Electrochemiluminescent label for DNA
Patent: US 5597910-A 9 28-JAN-1997;
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1 (bases 1 to 20)
Okazawa,K., Shimada,M., Katou,I., Fukushima,M.
DETECTION OF HUMAN PAPILLOMA VIRUS
Patent: JP 1993192200-A 26 03-AUG-1993;
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synthetic construct
artificial sequences.
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TAKARA SHUZO CO LTD
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C1201/70,C1201/68;
Strandedness: Single;
topology: Linear;
hypothetical: No;
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Artificial sequence; Genes.
JP 1993192200-A/26
03-AUG-1993
103-AUG-1993 JP 1991230839
20-AUG-1990 JP 90P 217067
20-AUG-1990 JP 90P 217067
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/mol_type="genomic DNA"
/db_xref="taxon:32630"
5 c 5 g
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              PAT 07-OCT-1997
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          J. Virol.
99214361
             Ai,W., Toussaint,E. and Roman,A. CCAAT displacement protein binds to and negatively papillomavirus type 6 E6, E7, and E1 promoters J. Virol. 73 (5), 4220-4229 (1999)
                                                                            Human papillomavirus type 6
Human papillomavirus type 6
Viruses; dsDNA viruses, no RNA stage;
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                                                                                                                                                                                                                                                                                                                                      1 (bases 1 to 30) Gudibande, S.R. and Kenten, J.H. Method for detecting a nucleic acid analyte using an electrochemiluminescent label Patent: US 5686244-A 9 11-NOV-1997;
                                                                                                                                                                                                                                                                                                                                                                                                      Unknown
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Gudibande, S.R. and Kenten, J.H.
Method for conducting a polymerase chain
electrochemiluminescent label
Patent: US 5610017-A 9 11-MAR-1997;
                                                                                                                                 Human papillomavirus type AF126428
                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 9 from 173213
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                                                                      Papillomavirus
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Similarity 100.0%;
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AR202652
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AR202651
Unknown.
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Direct Submission

Direct Submission

Direct Submitted (05-FEB-1999) Microbiology and Immunology,

University School of Medicine, 635 Barnhill Drive, Ir

46202-5120, USA
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Ai, W. and Roman, A.
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llarity 100.0%;
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SYAYKHLKVLEFRGGYPYAACACCLEFHCKINQYEHFDYAGYATTVEEETKQDILDVLI
RCYLCHKPLCEVEKVKHILTKARFIKLNCTWKGRCLHCWTTCMEDMLP"
144 c 145 g 175 t
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                                                                                                                                                                                                                                                          /organism="unknown"
269 c 213 g
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/mol_type="genomic DNA"
/strain="W50"
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AR202671
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                                                                                                                                                                                                                                                                                                                                                                                                    Webb, E.Ann., Margetts, M.Brigid., Cox, J.Cooper., McMillan, N.Alan. John., Williams, M.Philip., Moloney, M.Bridget. Holland. and Edwards, S. John. Papillomavirus polyprotein constructs Patent: US 6365160-A 23 02-APR-2002;
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                                                    1 (bases 1 to 4770)
Webb, E. Ann., Margetts, M. Brigid., Cox, J. Cooper. Webb, E. Ann., Margetts, M. Brigid., Cox, J. Cooper. Moloney, M. Bridget. Holland. and Edwards, S. John. Papillomavirus polyprotein constructs Patent: US 6365160-A 45 02-APR-2002;
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275 c 240 g
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331 c 283 g
         ∕organism="unknown"
890 c 1071 q
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1 TGCTAATTCGGTGCTACCTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Schwarz,E., Durst,M., Demankowski,C., Lattermann,O., Zech,R., Wolfsperger,E., Suhai,S. and zur Hausen,H.

DNA sequence and genome organization of genital human papillomavirus type 6b

EMBO J. 2 (12), 2341-2348 (1983)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                x00203.1 GI:60955
El gene; E2 gene; E4 gene; E5a gene; E5b gene; E6 gene; E7 gegene; L2 gene; major capsid protein L1; minor capsid protein regulatory protein E2; replication protein E1.
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Genital human papillomavirus type 6b (HPV6b).
X00203
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                                                          832. .2781
/gene="E1"
832. .2781
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                                                                                               /db_xref="SWISS-PROT:P06464"
/translation="MMGRHVTLKDIVLDLQPPDPVGLHCYEQLVDSSEDEVDEVDGQD
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RCYLCHKPLCEVEKVKHILTKARFIKLNCTWKGRCLHCWTTCMEDMLP"
                                                                                                                                                                                                                                                                                                                        530. .826
                                                                                                                                                                                                                                                                                                                                                                                                                     /codon_start=1
/product="E6 protein"
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/protein_id="CAA25019.1"
/db_xref="GI:60957"
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/strain="type 6b (HPV6b)"
/db_xref="taxon:10600"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Human papillomavirus
/mol_type="genomic DNA"
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                                     'gene="E1"
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/db_xref="SWISS-PROT: P03113"

/db_xref="SWISS-PROT: P06459"

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3887.
                                                                                                /gene="L2"
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AUTHORS
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FEATURES
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SOURCE
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Best Local Similarity
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Sequence 2 from patent US 6290965.
AR169144
                                                                                                                                                       DNA encoding human papillomavirus type Patent: US 6290965-A 2 18-SEP-2001; Location/Qualiflers
                                                                                                                                                                                                                  Unclassified.

1 (bases 1 to 8010)

Jansen, K.U. and Hofmann, K.J.
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1527 c 1718 g
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VLEDWNFGLSPPPNGTLEDTYRYVQSQAITCQKPTPEKEKPDPYKNLSFWEVNLKEKF
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MHPLVAAQDDT FDI Y AESFEPG I NPTQHPVTN I SDTYLTSTPNTYTQPWGNTTVPLSL
PNDLFLQSGPDI TFPTAPWGTPFSPVTPALPTGPVF I TGSGFYLHPAWY FARKRRKRI
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100.0%; Pred. No.
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I GI:940299
El gene; E2 gene; E4 gene; E5 gene; E6 gene; E7 gene; L
gene; complete genome.
Human papillomavirus type 6a
Human papillomavirus type 6a
Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hofmann, K.J., Cook, J.C., Joyce, J.G., Brown, D.R., Schultz, L.D., George, H.A., Rosolowsky, M., Fife, K. H. and Jansen, K. U. Sequence determination of human papillomavirus type 6a and assembly of virus-like particles in Saccharomyces cerevisiae virus-like particles in Saccharomyces cerevisiae virus-graphy 209 (2), 506-518 (1995)
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833. .835 is first start codon; putative"
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833. .2782
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531. .
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LVLVRFKVNKSRSTVARTLATLLNIPDNQMLIEPPKIQSGVAALYWFRTGISNASTVI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RCYLCHKPLCEVEKVKHILTKARFIKLNCTWKGRCLHCWTTCMEDMLP"
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103. .105 is first
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/gene="L1"
5790 .7700
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position 5790. .57
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3888. .4163
                                                                                                                                                                                                                                                               5/90. .7292
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /gene="E2"
2724 . .383
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FWLQPLVDAKVALLDDATQPCWIYMDTYMRNLLDGNPMSIDRKHKALTLIKCPPLLVT
SNIDITKEEKYKYLHTRVTTFTFPNPFPFDRNGNAVYELSNANWKCFFERLSSSLDIQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SIVSLIEESAIINAGAPEIVPPAHGGFTITSSETTTPAILDVSVTSHTTTSIFRNPVF
TEPSVTQPQPPVEANGHILISAPTITSHPIEEIPLDTFVISSSDSGPTSSTPVPGTAP
RPRVGLYSRALHQVQVTDPAFLSTPQRLITYDNPVYEGEDVSVQFSHDSIHNAPDEAF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TSTPVSSSTQEDAVQTPPRKRARGVQQSPCNALCVAHIGPVDSGNHNLITNNHDQHQR
RNNSNSSATPIVQFQGESNCLKCFRYKLNDKHRHLFDLISSTWHWASPKAPHKHAIVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /translation="MEAIAKRLDACQEQLLELYEENSTDLNKHVLHWKCMRHESVLLY
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CGQFKTYYVNFVKEAEKYGSTKQMEVCYGSTVICSPASVSSTTQEVSIPESTTYTPAQ
LGEHWGKGKQCTNTPVQAGDCPPLELITSVIQDGDMVDTGFGAMNFADLQTNKSDVPI
DICGTTCKYPDYLQMAADPYGDRLFFFLRKEQMFARHFFNRAGEVGEPVPDTLIIKGS
                                                    GHPYFSIKRANKTVVPKVSGYQYRVFKVVLPDPNKFALPDSSLFDPTTQRLVWACTGL
EVGRGQPLGVGVSGHPFLNKYDDVENSGSGGNPGQDNRVNVGMDYKQTQLCMVGCAPP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             position 3286.
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                                                                                                                                                                                                                                                                                                                                                                                PLFFSDVAA"
                                                                                                                                                                                                                                                                                                                                                                                                                                     MDIIRLHRPAIASRRGLYRYSRIGQRGSMHTRSGKHIGARIHYFYDISPIAQAAEEIE
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LKWGSLGVFFGGLGIGTGSGTGGRTGYVPLGTSAKPSITSGPMARPPVVVEPVAPSDP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /protein_id="AAA74217.1"
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/gene="E4"
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position 4424. .4426
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="base 3241 is first base after a stop codon; position 3286. .3288 is first start codon; putativ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /gene="E4"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    translation="MAAQLYVLLHLYLALHKKYPFLNLLHTPPHRPPPLCPQAPRKTQ"
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6 is first start codon; putativ
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start (
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putative"
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ORGANISM
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JOURNAL
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Kovelman,R., Bilter,G.K., Roman,A., Brown,D.R. and Barbosa,M.S. Human papillomavirus type 6: classification of clinical isolates and functional analysis of E2 proteins J. Gen. Virol. 80 (Pt 9), 2445-2451 (1999)
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Human
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AF092932
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (17-SEP-1998) Virology, Signal Pharmaceuticals, 5555 Oberlin Drive, San Diego, CA 92121, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Viruses;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Direct Submission
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VLEDWNFGLSPPPNGTLEDTYRYVQSQAITCQKPTPEKEKPDPYKNLSFWEVNLKEKF
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1 1527 c 1718 g 2295 t
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531. .827
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      no RNA stage; Papillomaviridae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Roman, A., Brown, D.R. and Barbosa, M.S.
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Search completed: August 23, 2003, 11:11:37 Job time: 997 secs

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MEDLINE
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VERSION
KEYWORDS
SOURCE
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                                                                                                                                                                                                                                                 TITLE
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Chambergo, F.S., Bonaccorsi, E.D., Ferreira, A.J.S., Ramos, A.S.P.,
Ferreira, J.R.Jr., Abrahao-Neto, J., Farah, J.P.S. and El-Dorry, H.
Elucidation of the metabolic fate of glucose in the filamentous
fungus Trichoderma reesei using expressed sequence tag (EST)
analysis and cDNA microarrays
J. Biol. Chem. 277 (16), 13983-13988 (2002)
                                                                                                           Hypocrea jecorina
Hypocrea jecorina
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1 (bases 1 to 670)
              Contact: El-Dorry, Hamza
Department of Blochemistry
Institute of Chemistry. University of Sao Paulo
Avenida Professor Lineu Prestes, 748, Sao Paulo,
                                                                                                                                                                            BM076659
Trest-A0592
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 (55) 11-38183848
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REFERENCE
AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                      Oryza sativa (japonica cultivar-group)
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 629)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AQ291095 629 bp DNA linear GSS 0 nbxb0038C14r CUGI Rice BAC Library Oryza sativa (japonica cultivar-group) genomic clone nbxb0038C14r, genomic surve
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Seq primer: M13 reverse primer
                                                                                                                                                                                             Tel: 864 656 7288
Fax: 864 656 4293
                                                                                                                                                                                                                                       Clemson University
100 Jordan Hall, C
                                                                                                                                                                                                                                                                                                                             Unpublished
                                                                                                                                                                                                                                                                                                                                             Wing, R.A. and Dean, R.A.

BAC End Sequencing Framework to Sequence the Rice Genome
                                                                                 High quality sequence stop: 481.
Location/Qualifiers
                                                                                                                                               Email: rwing@clemson.edu
Seq primer: GGAAACAGCTATGACCATG
                                                                                                                                                                                                                                                                               Clemson University Genomics Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Oryza sativa (japonica cultivar-group)
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                                                                                                                                                                                                                                                                                                         Contact: Wing RA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AQ291095.1 GI:3952385
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64 a 184 c 135 g 185 t 2 others
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/strain="QM9414 (ATCC26921)"
/db_xref="taxon:51453"
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                                                                                                                                                                                                                                     Clemson, SC 29634, USA
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0; Mismatches
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                                                                                                                                                                                                                                                                                 On Jan 28, 2002 this sequence version replaced gi:7709240 Contact: Arcaro MA, Morley M, Burdick J, Cheung VG Department of Pediatrics University of Pennsylvania 3516 Civic Center Blvd, ARC 516, Philadelphia, PA 19104, U
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                UP_309-16G_SP6 RPCI11 Human Male BAC Library Homo sapiens clone 309-16G, genomic survey sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cheung, V.G., Dalrymple, H.L., Narasimhan, S., Watts, J., Schuler, G., Raap, A.K., Morley, M. and Bruzel, A.
A resource of mapped human bacterial artificial chromosome clones Genome Res. 9 (10), 989-993 (1999)
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                                                                                                                                                                                                                                          Tel: 215 590 2664 Fax: 215 590 3709
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 831)
                                                                                                                                          Seq primer: SP6
Class: BAC ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AZ081985
                                                                                                                                                                                         Plate: 309
                                                                                                                                                                                                               Email: mlennox@mail.med.upenn.edu
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/note="Vector: pBeloBAC11; Site_1: HindIII; Site_2:
HindIII; Rice is one of two most popular grains in the
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/clone="309-16G"
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/lab_host="E. coli DH10B"
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                                                                                                                                                                                                                                                                                                                                                                                                                                               Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP brosophila melanogaster BAC ilbrary was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the 19 language of the BDGP's pland EST ilbraries. A more detailed description of the BDGP's and how to order individual BAC clones, the entire library, or filters for hybridization from the BACBAC Resource Center can be found at http://bacag.med.
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Drosophila melanogaster genome survey sequence TET3 end of BAC #
BACR20D02 of RPCI-98 library from Drosophila melanogaster (fruit
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fi
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/clone_lib="RPCI11 Human Male BAC Library"
/note="Vector: pBACe3.6; RPCI11 Human Male BAC Library"
189 c 174 g 242 t
                                                                                                                                                                                                                                                   /clone_lib="RPCI-98"
/note="end : TET3"
155 c 91 g
                                                                                                                                                                                                                                                                                                              /mol_type="genomic DNA"
/db_xref="taxon:7227"
/clone="BACR20D02"
                                                                                                                                                                                                                                                                                                                                                                         organism="Drosophila melanogaster"
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survey sequence TET3 end of BAC #
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Tingey,S.V., Poweli,W., Wolters,P., Dolan,M., Hainey,C., Yuan,Z., Miao,G., Caraher,N. and Hanafey,M.K.
DuPont Wheat cDNA Sequence
Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                 1 TGTCAAAAACCGTTGTGTCC 20
                                                                                                                                                  Triticum aestivum (bread wheat)
Triticum aestivum
                                                                                                                                                                                                                                                             CA620055 308 bp mRNA linear EST 23-NOV-2 wlln.pk0052.f8 wlln Triticum aestivum cDNA clone wlln.pk0052.f8
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                                                                                           Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
Triticeae; Triticum.
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                                                                                                                                                                                                                                               end, mRNA sequence.
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FORWARD: 5' GCCAAGCTCGAAATTAACCCTCACTAAAGGG 3'

BACKWARD: 5' CCAGTGAATTGTAATACGACTCACTATAGGGCG

Seq primer: 5' GAAATTAACCCTCACTAAAGGG 3'
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Identification and Characterization of Expressed Sequence Tags from an Embryonic Zebrafish Heart cDNA Library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ton, C., Mably, J.D., Dempsey, A.A., Hwang, D.M.,
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Danio rerio (zebrafish)
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5', mRNA servenen
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: cliew@rics.bwh.harvard.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   75 Francis St. Boston, MA 02115,
Tel: 6177328915
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Brigham and Women's Hospital
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AW454500.1 GI:6995287
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/lab_host="E.Coli xhl.Blue mrf'"
/clone_lib="Zebrafish Embryonic Heart cDNA Library"
/note="Organ: heart; Vector: Lambda ZAP Express; Site_1:
ECORI; Site_2: xho; mRNA was purified from embryonic
zebrafish hearts (3 day post-fertilization). cDNA was
synthesized using a XhoI-Oligo dT adaptor-primer. EcoRI
adaptors were ligated, followed by digestion with xhoI,
for directional cloning into pre-digested lambda ZAP
Express vector. "
01 a 56 c 61 g 79 t
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/mol_type="mRNA"
/db_xref="taxon:7955"
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90.0%;
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Pred. No. 3.8e+02;
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Ostariophysi; Cypriniform
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|||||||||||| ||| ||| 30 TGTCAAAAACCATTGTTTCC 11
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1 Innovation Way, P.O. Box 6104, Newark, DE 19714-6104, USA
Tel: 302-631-2602
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Stephen L. Johnson
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unpublished Other_ESTs: fv39c12.y1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BM103817 370 bp mRNA linear EST 21-NOV-201 fv39c12.x1 Sugano SJD adult male Danio rerio cDNA clone IMAGE:5410942 3' similar to SW:RPA5_HUMAN 0.15160 DNA-DIRECTED RNA POLYMERASE I 40 KD POLYPEPTIDE ;, mRNA sequence.
                                                                                                                                                                                             Consortium/LLNL, send email to: info@
Trace considered overall poor quality
High quality sequence stop: 1.
                                                                                                                                                                                                                                                                                                                            Email: zbrafish@watson.wustl.edu
Library constructed by Dr. Sumio Sugano and Dr. Koichi Kawakami DNA
Sequencing by: Washington University Genome Sequencing Center Clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WashU Zebrafish EST Project 1998
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1 (bases 1 to 370)
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                                                                                                                                                                                                                                                              distribution information can be found through the I Consortium/LLNL, send email to: info@image.llnl.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                Tel: 314 286 1800
Fax: 314 286 1810
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KOhn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R., Waterston,R.
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/tissue_type="leaf"
/tissue_type="leaf"
/clone_lib="w11n"
/clone_Teb="w11n"
/note="Vector: pBluescript SK+; Site_1: EcoRI; Site_2:
/note="Vector: pBluescript SK+; Site_1: EcoRI; Site_2: E
                           /organism="Danio rerio"
/mol_type="mRNA"
/db_xref="taxon:7955"
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/mol_type="mRNA"
/db_xref="taxon:4565"
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/clone="IMAGE:5410942"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Concordia University
1455 deMalsonneuve Blvd. West, Montreal, Quebec, CANADA, H3G 1M8
Tel: 514-848-3405
Fax: 514-848-4504
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tsang,A. and Storms,R. Aspergillus niger Expr Unpublished
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Aspergillus niger
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BACKWARD: GGCGTGAATGTAAGCGTGACATAAC
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Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
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//lab_host=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               tsang@vax2.concordia.ca
/clone_lib="Aspergillus niger, pYES2 (XhoI-EcoRI)"
/note="Yector: pYES2; Site_1: Xho-I; Site_2: EcoRI; cDNA
/note="Yector: pYES2; Site_1: Xho-I; Site_2: EcoRI; cDNA
was synthesized with ZhP kit (Stratagene) using poly(A)+
RNA isolated from Aspergillus niger grown in both complete
and minimal media. Synthesis was primed with oligo(dT)
primer/XhoI-linker. EcoRI adaptors were later ligated to
polished ends. EcoRI-XhoI-digested cDNA was ligated with
EcoRI-XhoI-digested pYES2 (Invitrogen Corp). This vector
permits expression of our library in yeast. "
                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Aspergillus niger"
/mol_type="mrNA"
/db_xref="taxon:5061"
/clone="1726"
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                                                                                                                                                                                                                                                                                                                                                                          /lab_host="E. coli"
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/tissue_type="whole body"
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Pred. No. 4
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4e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    425 bp mRNA linear EST 30-JAN-20 C0227A12-3 NIA Mouse 7.5-dpc Whole Embryo cDNA Library (Long) Mus musculus cDNA clone C0227A12 3', mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         National Institute on Aging/National Institutes of Health 333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA Email: cdna@lgsun.grc.nia.nih.gov Plate: C0227 row: A column: 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Piao, Y., Kargul, G.J., Dudekula, D.B., Qian, Y., Luo, A. and Ko, M.S.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Dawood B. Dudekula
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Systematic Analyses of NIA Mouse 7.5-dpc Whole Embryo cDNA Library
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Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mus musculus
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(bases 1 to 425)
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primer: -21M13 Forward
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           5'-pgAcTAGTTGCTAGATCGCGACCGCCCTTTTTTTTTTTT-3'] from
7' ug of total RNA, treated with T4 DNA polymerase, and
purified by ethanol-precipitation. The cDNAs were ligated
to Lone-linker L1-Sal4, purified by phenol/chloroform, and
separated from free linkers by Centricon 100. Then, the
cDNAs were amplified by long-range high fidelity PCR using
Ex Tag polymerase (Takara) with a primer Sal4-S. The
products were purified by phenol/chloroform and Centricon
100. The cDNAs were digested with Sal1 and Not1 enzymes
and cloned into Sal1/Not1 site of pSPORT1 plasmid vector.
                                                                                                                                                                                     /note-*Vector: psport1 (Invitrogen); Site_1: SalI; Site_2: NotI; Mouse cDNA project by the Laboratory of Genetics, National Institute on Aging (NIA), Intramural Research Program, NIH (http://lgsun.grc.nla.nih.gov/cDNA). This is a long-transcript enriched cDNA library (Ref: Genome Res. 11: 1553-1558 (2001). [PMID: 11544199]). Total RNAs were extracted from a pool of four embryos at 7.5-days postcoltum. Double-stranded cDNAs were synthesized with an Oligo(dT) primer [Invitrogen:
                                                                                                                                                                                                                                                                                                                                                                                                             /tissue_type="whole embryo including extraembryonic
tissues at 7.5-days postcoitum"
/dev_stage="7.5-days postcoitum"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /db_xref="niaEST:C0227A12-3"
/db_xref="taxon:10090"
/clone="C0227A12"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Mus musculus"
/mol_type="mRNA"
                                                                                                                                                                                                                                                                                                                                                                                       /clone_lib="NIA Mouse 7.5-dpc Whole Embryo cDNA Library
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 DH10B E.
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90.0%;
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coli host was transformed with the ligation
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Pred. No. 4.
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ches 2;
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                                                                                                                                                                                     Local
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                                                                                                                                                                                     Similarity
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234 TGTCAAAAACCCTTTTGTCC 253
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High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3618
Fax: (206) 616-3887
                                  1 TGTCAAAAACCGTTGTGTCC 20
                                                                                                                                                                                                                                                                                                                                                                                                            sequence Tagged Connector
Plate: 2020 row: K colu
Class: BAC ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence-tagged connectors: A sequence approach to mapping and scanning the human genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AQ228742 473 bp DNA linear GSS 26-S HS_2020_A2_F03_T7 CIT Approved Human Genomic Sperm Library D sapiens genomic clone Plate=2020 Col=6 Row=K, genomic survey
                                                                                                                                                                                                                                                                                                                                                                     High quality sequence stop: 473
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mahairas, G.G., Wallace, J.C., Smith, K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Keller, A., Shaker, R.,
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TGTCAAAAACCATAGTGTCC 187
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ing the human genome Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         jwallace@u.washington.edu
                                                                                                                                                                                      /clone_lib="CIT Approved Human Genomic Sperm Library /note="Organ: sperm; Vector: pBeloBAC11; BAC Clones i B-Coll DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     mixture by the standard chemical method. The average insert size is about 2.2 kb. The library was constructed by Yulan Piao (NIA). ^{\rm n} 87 c 76 g 118 t
                                                                                                                                                                                                                                                                                           /organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                      /sex="male"
                                                                                                                                                                                                                                                                          /clone="Plate=2020 Col=6 Row=K"
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90.0%;
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Pred. No. 4
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Pred. No. 4.1e+02;
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g,J., Zhao,S., Adams,M.D.
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508 bp

mRNA

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REFERENCE
AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sa44f10.y1 Gm-c1004 Glycine max cDNA clone GENOME SYSTEMS CLONE ID:
Gm-c1004-2180 5' similar to TR:Q96502 Q96502 COL2. ;, mRNA
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Glycine max (soybean)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Shoemaker R/Public Soybean EST Project
Public Soybean EST Project
Washington University School of Medicine
4444 Porest Park Parkway, Box 8501, St. Louis, MO 63108, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ,R., Waterston,R. and Wilso
Public Soybean EST Project
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Fax: 314 286 1810
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                   quality
520-523-7500, email: paul.keim@nau.edu, virginia.coryell@nau.edu"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Glycine max'
/mol_type="mRNA"
/db_xref="taxon:3847"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                  /clone_lib="Gm-c1004"
                                                                                                                                                                                                                                                                                                                                                                                                                               /lab_host="XL10-Gold"
                                                                                                                                                                                                                                                                                                                                                                                                                                             /tissue_type="root"
                                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone="GENOME SYSTEMS CLONE ID: Gm-c1004-2180"
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Beck,C.,
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BI830009
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Crop Genetics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unpublished
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BASE COUNT
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidea
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              E. I. DuPont de Nemours and Company
1 Innovation Way, P.O. Box 6104, Newark,
Tel: 302-631-2602
                           Homo sapiens (human)
                                                                                                          BI830009
603080272F1 NIH_MGC_119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tingey,S.V., Powell,W., Wolters,P., Miao,G., Caraher,N. and Hanafey,M.K.
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                                                                   BI830009.1 GI:15941559
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Fax: 302-631-2607
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Scott V. Tingey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DuPont Wheat cDNA Sequence
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                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Scott. V. Tingey@USA.dupont.com
                                                                                                                                                                                                                                                                                                                                  XhoI; Wheat (Triticum aestivum L.) root;
wrel library"
                                                                                                                                                                                                                                                                                                                                                             /clone="wre1n.pk0094.c4"
/tlssue_type="root"
/clone_lib="wre1n"
/note="Vector: pBluescript SK+; Site_1: EcoRI; Site_2:
                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Triticum aestivum"
/mol_type="mRNA"
/db_xref="taxon:4565"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
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No. 4.3e+02;
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                                                                                                           sapiens cDNA clone IMAGE:5171968 5',
Craniata; Vertebrata; Catarrhini; Hominidae
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              Euteleostomi;
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AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                AGENCOURT_10554416 NIH_MGC_127 Homo sapiens cDNA clone IMAGE:6713986 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         18;
                                                                                                                                                                                                                                           1 (bases 1 to 875)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                          EST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Robert Strausberg, Ph.D.
                               CDNA Library Preparation: Michael Brownstein Laboratory CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Agencourt Bioscience Corporation Clone distribution: MGC clone distribution information can found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov plate: LiCM3025 row: c column: 10
                                                                                                                                                                     Email: cgapbs-r@mail.nih.gov
Tissue Procurement: NCI
                                                                                                                                                                                                           Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
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BU941677.1
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Plate: LLAM11427 row: p column:
High quality sequence stop: 653.
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National Institutes of Health, Mammalian Gene Collection (MGC)
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                 quality sequence stop: 302
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Site_2: EcoRV (destroyed); RNA source normal medulla from anonymous male age 27. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.3 kb, insert size range 0.9-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 013. Note: this is a NIH_MGC Library."

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/db_xref="taxon:9606"
/clone="IMAGE:5171968"
Location/Qualifiers
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'lab_host="DH10B"
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Pred. No. 4.5e+02;
0; Mismatches 2;
                                                                                                                                                                                                                                                                                                        Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
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Query Match
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                                                                                                                                                                                                          Plate: LLCM1219 row: 1 column: High quality sequence start: 2 High quality sequence stop: 686.
                                                                                                                                                                                                                                                                                         found through the I.M.A.G.E. Consortium/LLNL http://image.llnl.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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1. (bases 1 to 929)
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BG335280
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Unpublished
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                                                                                                                                                                                                                                                                                                                                              CDNA Library Preparation: Ling Hong/Rubin Laboratory CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution information can
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens (human)
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5'-AACCAGTGGTATCAACGCAGAGTGGCCATTACGGCCGG-3' and a coloning as follows:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5'-ATTCTAGAGGCCGAGGCGGCCGACATG-dT(30)NN-3'. Full-length enriched library was constructed using the Clontech Creator SMART kit and size-selected to contain the 1-2 kb size fraction (other fractions present in NIH_MGC_126 and NIH_MGC_128). Library created in the laboratory of T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Library."
193 c
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                                                                         /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
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/lab_host="DH10B (T1-phage-resistant)"
/clone_lib="NIH_MGC_127"
/note="Vector: pDNR-LIB; Site_1: Sfil (ggccattatggcc);
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/mol_type="mRNA"
/tissue_type="choriocarcinoma"
/lab_host="DH10B (phage-resistant)"
                                                                                                                                                                                 Location/Qualifiers
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                                                      /clone="IMAGE:4541350"
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Pred. No. 4.8e+02;
D; Mismatches 2;
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BASE COUNT
ORIGIN
Search completed: August 23, 2003, 12:13:20 Job time: 1851 secs
                                                                                                                                                                                                                             Query Match 84.0%; Score 16.8; DB 10; Length 929; Best Local Similarity 90.0%; Pred. No. 4.8e+02; Matches 18; Conservative 0; Mismatches 2; Indels 0;
                                                                                                           /clone_lib="NIH_MGC_21"
/note="Organ: placenta; Vector: pOTB7; Site_1: XhoI;
Site_2: EcoRi; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-CDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."

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Maximum Match 100%
Listing first 45 summaries
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    length: 0
length: 2000000000
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Gapop 10.0 , Gapext 1.0
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: /cgn2_6/ptodata/1/pubpna/USOB_NEW_PUB.seq:*
: /cgn2_6/ptodata/1/pubpna/USOB_NEW_PUB.seq:*
: /cgn2_6/ptodata/1/pubpna/USOB_PUBCOMB.seq:*
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: /cgn2_6/ptodata/1/pubpna/USO9C_PUBCOMB.seq:*
2: /cgn2_6/ptodata/1/pubpna/USO9_NEW_PUB.seq:*
3: /cgn2_6/ptodata/1/pubpna/USOB_NEW_PUB.seq:*
4: /cgn2_6/ptodata/1/pubpna/USOB_NEW_PUB.seq:*
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6: /cgn2_6/ptodata/1/pubpna/USOB_NEW_PUB.seq:*
6: /cgn2_6/ptodata/1/pubpna/USOB_NEW_PUB.seq:*
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/cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
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/cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*
/cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*
  GenCore version 5.1.6 (c) 1993 - 2003 Compugen Ltd
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    US-10-286-387-8
US-10-292-848-18
US-10-296-387-9
US-10-286-387-10
US-10-286-387-13
US-10-128-714-2427
US-10-128-714-6427
US-10-128-714-6427
US-10-128-714-5427
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US-10-286-387-15
US-09-941-492-119
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				Sequence 25868, A		Sequence 207791,		Sequence 1753, Ap	e 8841,	•	Sequence 270, App	e 1	Ŋ	Ļ	Ņ	Sequence 1, Appli	Ņ	-	Sequence 5, Appli	ø	ω	Sequence 3, Appli		Sequence 191550,		Sequence 184710,	Sequence 10792, A	Sequence 6139, Ap

## ALIGNMENTS

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US-10-292-848-18
Sequence 18, Application US/10292848
Publication No. US20030119042A1
GENERAL INFORMATION:
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US-10-286-387-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 8, Application US/10286387

Publication No. US20030143529A1

GENERAL INFORMATION:
APPLICANT: Cytyc Corporation

TITLE OF INVENTION: Detection and Typing of Human Papillomavirus Using PNA Probes

FILE REFERENCE: cym-035CP

CURRENT APPLICATION UNMEER: US/10/286,387

CURRENT FILING DATE: 2003-02-28

NUMBER OF SEQ ID NOS: 31

SOCTWARE: PATENTIN Version 3.1

SEQ ID NO 8

LENGTH: 20

PAUSE: NA
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Best Local (
APPLICANT: ROSADO, Pedro M.
APPLICANT: LOPEZ, Gemma L.
APPLICANT: SEIZ, Antonio M.
APPLICANT: ALBERDI, Maria D.
APPLICANT: ALBERDI, Maria D.
TITLE OF INVENTION: Method for preparing stabilized reaction mixtures, which are t
                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Artificial FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA
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Pred. No. 0.73;
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US-10-286-387-9
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SEQ ID NO 18
LENGTH: 20
                                                                                                                                                                            Sequence 10, Applica Publication No. US20 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQ ID NOS: 31
SOFTWARE: PatentIn version 3.1
SEQ ID NO 9
LENGTH: 23
                             NUMBER OF SEQ ID NOS: 31
SOFTWARE: Patentin version 3.1
SEQ ID NO 10
LENGTH: 23
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                                                                                            APPLICANT: Cytyc Corporation
TITLE OF INVENTION: Detection and Typing of Human Papillomavirus Using PNA Probes
FILE REFERENCE: cym-035CP
CURRENT APPLICATION NUMBER: US/10/286,387
CURRENT FILING DATE: 2003-02-28
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: PCT/ES02/00109
PRIOR FILING DATE: 2002-3-11
PRIOR APPLICATION NUMBER: ES P0100569
PRIOR FILING DATE: 2001-3-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Cytyc Corporation
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ORGANISM: Artificial
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA
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. OTHER INFORMATION: Forward primer used to amplify region of E6 US-10-286-387-10 \,
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SOFTWARE: Pate
SEQ ID NO 2427
LENGTH: 1409
TYPE: DNA
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SOFTWARE: PatentIn version 3.1
SEQ ID NO 13
LENGTH: 23
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Publication No.
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                                                                                                                 PRIOR APPLICATION NUMBER: US 60/287,066
PRIOR FILING DATE: 2001-04-27
PRIOR APPLICATION NUMBER: US 60/295,890
PRIOR FILING DATE: 2001-06-05
PRIOR APPLICATION NUMBER: US 60/303,899
PRIOR FILING DATE: 2001-07-09
                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/10/128,714
CURRENT FILING DATE: 2002-04-23
PRIOR APPLICATION NUMBER: US 60/285,697
PRIOR FILING DATE: 2001-04-23
                                                                                                                                                                                                                                                                                       APPLICANT: Hu, Wenqi
APPLICANT: Tishkoff, Daniel
APPLICANT: Zamudio, Carlos
APPLICANT: Zamudio, Carlos
APPLICANT: Lenieux, Sebastien M
APPLICANT: Lenieux, Sebastien M
TITLE OF INVENTION: Identification of Essential Genes
TILE OF INVENTION: Methods of Use
FILE REFERENCE: 10182-018-999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/10/286,387
CURRENT FILING DATE: 2003-02-28
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TITLE OF INVENTION: Detection and Typing of Human Papillomavirus Using PNA Probes
FILE REFERENCE: cym-035CP
                                                                                   PRIOR FILING DATE:
                                                                                                   PRIOR APPLICATION NUMBER: US 60/316,362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Artificial
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No. US20030143529A1
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APPLICANT: Jiang, Bo
APPLICANT: Hu, Wenq1
APPLICANT: Hishkoff, Daniel
APPLICANT: Zamudio, Carlos
APPLICANT: Zamudio, Carlos
APPLICANT: Lemieux, Sebastien M
APPLICANT: Lemieux, Sebastien M
TITLE OF INVENTION: Identification of Essential Genes in
TITLE OF INVENTION: Methods of Use
FILE REFERENCE: 10182-018-999
CURRENT APPLICATION NUMBER: US/10/128,714
CURRENT FILING DATE: 2002-04-23
CURRENT FILING DATE: 2002-04-23
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US-10-128-714-6427/c
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US-10-128-714-7427/c
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CURRENT FILING DATE: 2002-04-23
PRIOR APPLICATION NUMBER: US 60/285,697
PRIOR FILING DATE: 2001-04-23
PRIOR APPLICATION NUMBER: US 60/287,066
PRIOR FILING DATE: 2001-04-27
PRIOR APPLICATION NUMBER: US 60/295,890
PRIOR APPLICATION NUMBER: US 60/295,890
PRIOR FILING DATE: 2001-06-05
PRIOR APPLICATION NUMBER: US 60/303,899
PRIOR FILING DATE: 2001-07-09
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Best Local
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PRIOR FILING DATE: 2001-08-31
NUMBER OF SEQ ID NOS: 8603
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APPLICANT: Zamudio, Carlos
APPLICANT: Eroshkin, Alexey M
APPLICANT: Lemieux, Sebastien M
TITLE OF INVENTION: Identification of Essential Genes in Aspergillus fumigatus and
TITLE OF INVENTION: Methods of Use
FILE REFERENCE: 10182-018-999
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APPLICANT: Hu, Wengi
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hes 17; Conservation
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    APPLICATION NUMBER: US 60/285,697 FILING DATE: 2001-04-23
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Pred. No. 2
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Pred. No. 2.2e+02;
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RESULT 10
US-10-128-714-5427/c
; Sequence 5427, Application US/10128714
; Publication No. US20030119013A1
; GENERAL INFORMATION:
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; SEQ ID NO 6427
; LENCTH: 1518
; TYPE: DNA
; ORGANISM: Aspergillus fumigatus
US-10-128-714-6427
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TYPE: DNA
; ORGANISM: Aspergillus fumigatus
US-10-128-714-1427
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SOFTWARE: Paten
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Best Local :
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APPLICANT: Hu, Wengi
APPLICANT: Tishkoff, Daniel
APPLICANT: Zamudio, Carlos
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PRIOR FILING DATE: 2001-06-05
PRIOR APPLICATION NUMBER: US 60/303,899
PRIOR FILING DATE: 2001-07-09
PRIOR APPLICATION NUMBER: US 60/316,362
PRIOR FILING DATE: 2001-08-31
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PRIOR APPLICATION NUMBER: US 60/295,890
PRIOR FILING DATE: 2001-06-05
PRIOR APPLICATION NUMBER: US 60/303,899
PRIOR FILING DATE: 2001-07-09
PRIOR APPLICATION NUMBER: US 60/316,362
PRIOR FILING DATE: 2001-08-31
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PRIOR FILING DATE: 2001-04-23
PRIOR APPLICATION NUMBER: US 60/287,066
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CURRENT APPLICATION NUMBER: US/10/128,714
CURRENT FILING DATE: 2002-04-23
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APPLICANT: Lemieux, Sebastien M
TITLE OF INVENTION: Identification of Essential Genes in Aspergillus fumigatus
TITLE OF INVENTION: Methods of Use
                                                                                                                                                                                                                                            NUMBER OF SEQ ID NOS: 8603
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878 GCCAAAAACCCTTGTGTCC
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Pred. No. 2.
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Pred. No. 2
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US-10-128-714-427/c
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CURRENT APPLICATION NUMBER: US/10/128,714
CURRENT FILING DATE: 2002-04-23
PRIOR APPLICATION NUMBER: US 60/285,697
PRIOR FILING DATE: 2001-04-23
PRIOR APPLICATION NUMBER: US 60/287,066
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PRIOR FILING DATE: 2001-04-23
PRIOR APPLICATION NUMBER: US 60/287,066
PRIOR FILING DATE: 2001-04-27
PRIOR APPLICATION NUMBER: US 60/295,890
PRIOR APPLICATION NUMBER: US 60/295,890
PRIOR FILING DATE: 2001-06-05
PRIOR FILING DATE: 2001-06-05
PRIOR FILING DATE: 2001-08-31
PRIOR APPLICATION NUMBER: US 60/316,362
PRIOR APPLICATION NUMBER: US 60/316,362
PRIOR APPLICATION NUMBER: US 60/316,362
PRIOR FILING DATE: 2001-08-31
                                                                                           SOFTWARE: Pate
SEQ ID NO 427
LENGTH: 3520
TYPE: DNA
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SEQ ID NO 5427
LENGTH: 3518
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CURRENT APPLICATION NUMBER: US/10/128,714
CURRENT FILING DATE: 2002-04-23
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Tishkoff, Daniel
Zamudio, Carlos
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Lemieux, Sebastien M
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Lemieux, Sebastien M
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    Score 15.8;
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US-10-286-387-15
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                                                                                          SOFTWARE: Fa
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION
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                                                                                                                                                                                                                                                                                                                                          CURRENT FILING DATE: 2002-04-01
PRIOR APPLICATION NUMBER: 09/838,858
PRIOR FILING DATE: 2001-04-20
                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Puttaraju, Madaiah
APPLICANT: Mansfield, Gary S.
TITLE OF INVENTION: METHODS OF COMPOSITIONS FOR USE
TITLE OF INVENTION: SPLICEOSOME MEDIATED RNA TRANS-
FILE REFERENCE: A31304-BAE (072874.0156)
CURRENT APPLICATION UNDMERS: US/09/941,492
CURRENT FILING DATE: 2002-04-01
                                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: 09/133,717 PRIOR FILING DATE: 1998-08-13
                                                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: 09/158,863 PRIOR FILING DATE: 1998-09-23
                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: 09/756,096
PRIOR FILING DATE: 2001-01-08
                                                                                                                                 NUMBER OF SEQ ID NOS:
                                                                                                                                                     PRIOR FILING DATE:
                                                                                                                                                                                                        PRIOR APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Mitchell,
                 ORGANISM: Artificial Sequence FEATURE:
                                                         TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OTHER INFORMATION: Forward primer used to amplify region of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Artificial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA
OTHER INFORMATION: Binding domain of human papilloma virus PTM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local
                                                                                                                                                                   APPLICATION NUMBER: 08/766,354
                                                                                                                                                                                       FILING DATE: 1998-05-28
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17; Conserv
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                                                                                                                FastSEQ for Windows Version
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85.0%;
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Pred. No. 2
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US-09-918-995-33830/c
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                                                                                                                                                                                                                             Sequence 33830, Application US/09918995
publication No. US20030073623A1
GENERAL INFORMATION:
APPLICANT: Hyseq, Inc.
TITLE OF INVENTION: FROM VARIOUS CDNA LIBRARIES
FILE REFERENCE: 20411-756
CURRENT FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: US/09/235,076
PRIOR FILING DATE: 1999-01-20
NUMBER OF SEC IN NOS-23664
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 122 LENGTH: 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
                                                                           NUMBER OF SEQ ID NOS: 38054
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 33830
LENGTH: 431
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PRIOR FILING DATE: 2001-04-20
PRIOR APPLICATION NUMBER: 09/756,096
PRIOR FILING DATE: 2001-01-08
PRIOR APPLICATION NUMBER: 09/158,863
PRIOR FILING DATE: 1998-09-23
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APPLICANT: Mansfield, Gary S.
TITLE OF INVENTION: WETHODS OF COMPOSITIONS FOR USE IN
TITLE OF INVENTION: SPLICEOSOME MEDIATED RNA TRANS-SPLICING
FILE REFERENCE: A31304-BAE (072874.0156)
CURRENT APPLICATION NUMBER: US/09/941,492
CURRENT FILING DATE: 2002-04-01
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PRIOR FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: 09/087,233
PRIOR FILING DATE: 1998-05-28
PRIOR APPLICATION THE PRIOR OF THE PRIOR APPLICATION TO THE PR
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ORGANISM: Homo sapiens
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Pred. No. 2.9e+02;
0; Mismatches 3;
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Pred. No. 3.1e+02;
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US-09-918-995-33830
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Query Match 76.0%; Score 15.2; DB 11; Length 431; Best Local Similarity 85.0%; Pred. No. 3.7e+02; Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps

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Search completed: August 23, 2003, 13:53:16 Job time: 147 secs

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score:

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Post-processing: Minimum Match 0%
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1: /cgn2_6/ptodata/2,
2: /cgn2_6/ptodata/2,
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/cgn2_6/ptodata/2/ina/backfiles1.seq:*
                      US-08-495-743-27
US-08-495-739-27
US-08-062-023-27
US-08-062-023-27
US-09-056-105-29
US-09-359-382-11
US-09-369-751-71
PCT-US94-05085-1
PCT-US94-05085-1
US-09-369-751-71
PCT-US94-05085-1
US-09-210-168-3
US-08-216-233C-1
US-09-210-168-3
US-09-485-885-3
US-09-485-885-3
US-09-485-885-3
US-09-485-885-13
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US-08-495-743-27/c
US-08-495-743-27/c
Application
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MEDIUM TYPE: Diskette, 3.5inch, 1.4
COMPUTER: IBM PS/2
OPERATING SYSTEM: MS-DOS Version 3.
SOFTWARE: PC-8 (Word for Windows)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/495,743
FILLING DATE: 08-JUN-1995
CLASSIFICATION: 435
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                                                                                                                                                                                            TELEFAX: (716) 477-4646 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
                    MOLECULE TYPE:
HYPOTHETICAL: I
ANTI-SENSE: NO
                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/062,023
FILING DATE: 14-MAY-1993
ATTORNEY/AGENT INFORMATION:
NAME: Tucker, J. Lanny
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REGISTRATION NUMBER: 27,678
REFERENCE/DOCKET NUMBER: 677
TELECOMMUNICATION INFORMATION:
TELEPHONE: (716) 722-9332
                                                                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 29 nucleotides
  ORIGINAL SOURCE:
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                                                                                STRANDEDNESS:
TOPOLOGY: Lir
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ZIP: 14650 - 2201
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DEDNESS: Single
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343 State Street
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Lynn Bergmeyer, John B. Findlay
John W.H. Sutherland, JoAnne H. Kerschner
VERVION: DIAGNOSTIC COMPOSITIONS, ELEMENT-
VERTION: METHODS AND TEST KITS FOR
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US-08-313-238-53
US-08-819-177-2
US-08-18-228-41
US-08-332-638-41
US-08-332-638-41
US-08-316-239B-1
US-08-316-239B-1
US-08-316-239B-2
US-08-316-239B-2
US-08-316-239B-2
US-08-316-239B-2
US-08-316-239B-2
US-08-316-239B-2
US-08-316-239B-2
US-09-140-1
US-09-531-857A-1
US-09-531-857A-1
US-09-09-094-19
US-09-000-094-21
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IMMEDIATE SOURCE: Same PUBLICATION INFORMATION: No. US-08-495-739-27
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Best Local Similarity
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION:
                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 29 nucleotides
                                                                                                                                                                                                                                                                                                                       NAME: Tucker, J. Lanny
REGISTRATION NUMBER: 27,678
REFERENCE/DOCKET NUMBER: 67
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 14 MAY 1993 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OPERATING SYSTEM: MS-D
SOFTWARE: PC-8 (Word f
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
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                                                                                                                                                              ANTI-SENSE:
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HYPOTHETICAL:
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CLASSIFICATION: 435
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17; Conserv
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14650 - 2201
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Lynn Bergmeyer, John B. Findlay
John W.H. Sutherland, Johnne H. Kerschner
VENTION: DIAGNOSTIC COMPOSITIONS, ELEMENT
VENTION: METHODS AND TEST KITS FOR
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Same
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85.0%;
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Pred. No. 3
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RESULT 4
US-08-062-023-27/c
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US-08-495-741-27/c
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Sequence 27, Application US/08062023 Patent No. 6174668
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                                                                                                                                                        Matches
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                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: (716) 477-4646
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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APPLICANT:
                                                                                                                                                                                                                                                          HYPOTHETICAL: NO ANTI-SENSE: NO. ORIGINAL SOURCE: Synthetically prepared
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION: 435
PRIOR APPLICATION DATA:
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CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                          MOLECULE TYPE:
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                                                                                                                                                                                                                                                 IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Tucker, J. Lanny REGISTRATION NUMBER: 27, REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 19
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/0: FILING DATE: 08-JUN-1995
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER:
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TRY: U.S.A.
14650 - 2201
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17; Conserv
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343 State Street
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John W.H. Sutherland, JoAnne H. Kerschner
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85.0%;
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lord for Windows)
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Pred. No. 36;
0; Mismatches
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GENERAL INFORMATION:

APPLICANT:

Thomas

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Cummins, Susan M.

Atwood

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Best Local Similarity. 85.0
17; Conservative
                                                                                                                                                                                                                     Patent No. 6287569
                                                                                                                                                                                                   GENERAL INFORMATION:
                                TITLE OF INVENTION: VACCINES WITH ENHANCED INTRACELLULAR TITLE OF INVENTION: PROCESSING FILE REFERENCE: 235/221
CURRENT APPLICATION NUMBER: US/09/056,105
CURRENT FILING DATE: 1998-04-06
EARLIER APPLICATION NUMBER: 60/043,467
EARLIER FILING DATE: 1997-04-10
                                                                                                                                                             APPLICANT: KIPPS, THO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: (716) 477-4646
INFORMATION FOR SEQ ID NO: 5
SEQUENCE CHARACTERISTICS:
LENGTH: 29 nucleotides
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REFERENCE/DOCKET NUMBER: 67271A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (716) 722-9332
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PS/2
OPERATING SYSTEM: MS-
SOFTWARE: PC-8 (Word
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: UFILING DATE: 19930514
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Diskette, 3.5inch, 1:44 MB storage (IBM)
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14650 - 2201
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                     SEQ ID NOS:
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                                                                                                                                                                                                                                    Application US/09056105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3: Eastman Kodak Company, Patent Legal Staff
343 State Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         John
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Linear
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for Windows Version 3.0
                                                                                                                                                                                    THOMAS J
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W.H. Sutherland, JoAnne H. Kerschner
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                                                                                                                                                                                                                                                                                                                                                                                                                         76.0%;
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Pred. No. 3
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; SEQ ID NO 29
; LENGTH: 456
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-056-105-29
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Best Local Similarity
Matches 17; Conserv
                                                                                                SEQ ID NO 11
LENGTH: 519
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CURRENT FILING DATE: 1999-10-29
PRIOR APPLICATION NUMBER: 60/106,495
PRIOR FILING DATE: 1998-10-30
NUMBER OF SEQ ID NOS: 8
                                                                                                                                              EARLIER APPLICATION NUMBER: AU PN0157
EARLIER FILING DATE: 1994-12-20
NUMBER OF SEQ ID NOS: 15
                                                                                                                                                                                                                                                                   APPLICANT: WEBB, Elizabeth Ann
APPLICANT: FRAZER, IAN
TITLE OF INVENTION: VARIANTS OF HUMAN PAPILLOMA VIRUS ANTIGENS
FILE REFERENCE: 17227/130
                                                                                                                                                                                                                                                                                                                                APPLICANT: EDWARDS, Stirling John APPLICANT: COX, John Cooper
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APPLICANT: Crish, James F.
TITLE OF INVENTION: Tissue Specific Promoters and Transgenic Animals
TITLE OF INVENTION: the Screening of Pharmaceuticals
FILE REFERENCE: CASE-04022
                                                                                                                                                                                                   EARLIER APPLICATION NUMBER: PCT/AU95/00868 EARLIER FILING DATE: 1995-12-20
                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/08/860,165A CURRENT FILING DATE: 1997-09-22
                                                                                                                                  SOFTWARE: PatentIn Ver.
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                                                      TYPE: DNA
ORGANISM: Artificial Sequence
          NAME/KEY: CDS
LOCATION: (1)..(516)
FEATURE:
                                                 FEATURE:
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85.0%;
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Pred. No. 5
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Pred. No. 51;
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Query Match Best Local Matches 1

Similarity

76.0%; 85.0%;

Score 15.2; Pred. No. 52;

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Length 525; Indels

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Pred. No. 52; ); Mismatches

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; NAME/KEY: CDS
; LOCATION: (1)..(516)
US-09-359-382-11
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Best Local
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                                                                      SEQ ID NO 71
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TYPE: DNA
ORGANISM: Drosophila
-09-669-751-71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
                                                                                                                                                         APPLICANT: Greenspan, Ralph J.
TITLE OF INVENTION: Methods for Identifying Compounds for TITLE OF INVENTION: Method Sickness, Vertigo and Other Dir TITLE OF INVENTION: Balance and the Perception of Gravity FILE REFERENCE: P-NI 3864
CURRENT EPPLICATION NUMBER: US/09/669,751
CURRENT FILING DATE: 2000-09-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION NUMBER: US/09/359,382 CURRENT FILING DATE: 1999-07-23 EARLIER APPLICATION NUMBER: US 08/860,165 EARLIER FILING DATE: 1997-09-22 EARLIER APPLICATION NUMBER: PCT/AU95/00868 EARLIER FILING DATE: 1995-12-20
                                                                                        SOFTWARE:
                                                                                                                        PRIOR APPLICATION NUMBER: US PRIOR FILING DATE: 1999-12-02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EARLIER APPLICATION NUMBER: AU PN0157/94
EARLIER FILING DATE: 1994-12-20
NUMBER OF SEQ ID NOS: 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: WEBB, Elizabeth Ann
APPLICANT: FRAZER, Ian
TITLE OF INVENTION: VARIANTS OF HUMAN PAPILLOMA VIRUS ANTIGENS
FILE REFERENCE: 017227/0148
                                                                                                        NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: EDWARDS, Stirling John APPLICANT: COX, John Cooper
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA ORGANISM: Human papillomavirus type
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                                                      LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local
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                                                                                        FastSEQ for Windows Version 4.0
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Pred. No. 5
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Pred. No. 52;
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                                   Matches
                                                                 Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: 708/948-2642 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                               ANTI-SENSE: no ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                            HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION: PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: HUMAN PAPILLOMAVIRUS DETECTION ASSAY NUMBER OF SEQUENCES: 44
                                                                                                                                                                                                                                                   PUBLICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: BA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US 0 FILING DATE: May 6, 1993 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION DATA:
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                                                                                                                                                    AUTHORS: Seedori, A., ... AUTHORS: Suhai, S., and Rowekamp, W.
AUTHORS: Human Papillomavirus Type 16 DNA Sequence
JOURNAL: Virology
                                                                                                                                                   VOLUME:
                                                  Local Similarity
                                                                                                                  PAGES: 181-185
DATE: 1985
                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: nucleic acid
STRANDEDNESS: doub
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OPERATING SYSTEM: Apple Macintosh System 7.0 SOFTWARE: Macintosh Text File
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COMPUTER: Apple Macintosh
OPERATING SYSTEM: Apple M
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STREET: One Baxter Parkway, Building DP-3E
CITY: Deerfield
                                                                                                                                                                                                                                                                                                                   ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                NAME/KEY: Portion of viral genome coding
                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY:
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   1 TGTCAAAAACCGTTGTGTCC 20
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Mark Buonaiuto
31,593
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                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                  linear
                                                                                                                                                                                                                                                                                                                Papaoviridae, Human papilloma virus
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85.0%;
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                                   0; Mismatches
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                                                 Score 15.2;
Pred. No. 53;
                                                                     DB
                                                                                                                                                                                                                                                                  for E6/E7 polypeptides.
                                                                   5.
                                                                 Length 570;
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TGTCAAAAGCCACTGTGTCC

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APPLICANT:

HAYDOCK, PAUL V.

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RESULT 12
US-08-216-233C-1
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              Sequence 1, Application US/08216233C Patent No. 5506105
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GENERAL INFORMATION:
APPLICANT: Janice T. Brown
                                                                                                                                                                            Matches
                                                                                                                                                                                        Query Match
Best Local S
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Mark Buonaluto
REGISTRADIO NUMBER: 31,593
REFERENCE/DOCKET NUMBER: BA
TELECOMMUNICATION INFORMATION:
TELEPHONE: 708/948-2537
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: May 6, 1993 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Macintosh Te
                                                                                                                                                                                                                                                                                                                                                                                    PUBLICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
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VOLUME: 145
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TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Apple M
                                                                                                                                                                                                                                                         PAGES: 181-185
DATE: 1985
                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN: 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION:
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                                                                                                             338 TGTCAAAAGCCACTGTGTCC 357
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Human Papillomavirus Type 16 DNA Sequence
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One Baxter Parkway, Building DP-3E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     USA
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                                                                                                                                                                                                                                                                                                                                                                                                 Portion of viral genome coding for E6/E7 polypeptides
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                                                                                                                                                                                                                                                                                                                     Virology
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85.0%;
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Pred. No. 53
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; OTHER INFORMATION: E6/E7-HPV16
JS-09-210-168-3
                                                                                           SEQ ID NO 3
LENGTH: 779
                                                                                                                 PRIOR APPLICATION NUMBER: U.S. 60/070,486
PRIOR APPLICATION NUMBER: U.S. 60/069,426
PRIOR FILING DATE: 1997-12-12
NUMBER OF SEO ID NOS: 5
SOFTWARE: Patentt.
                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION: APPLICANT: Lorincz
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Best Local Similarity 85.0%;
Matchès 17; Conservative
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                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/09/210,168 CURRENT FILING DATE: 1998-12-11 PRIOR APPLICATION NUMBER: U.S. 60/082,167 PRIOR EILING DATE: 1998-04-17 PRIOR APPLICATION NUMBER: U.S. 60/070,486 PRIOR FILING DATE: 1998-01-05
                                                                                                                                                                                                                                                                                                                      FILE REFERENCE:
                                                                                                                                                                                                                                                                                                                                   APPLICANT: LOTINCZ, Attila T. TITLE OF INVENTION: ASSESSMEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: (305) 222-66 INFORMATION FOR SEQ ID NO:
                                                  ORGANISM: Human papillomavirus
                                 FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/216,233C
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LENGTH: 776 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REGISTRATION NUMBER: 34,745
REFERENCE/COCKET NUMBER: BA 4203
TELECOMMUNICATION INFORMATION:
TELEPHONE: (305) 222-6423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/808,456
FILING DATE: 10-DEC-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: DNA (genomic)
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MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: FILING DATE: 22-MAR
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1717 DEERFIELD ROAD
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                                                                                                                                                                                                                                                                                                                                     ASSESSMENT OF HUMAN PAPILLOMA VIRUS-RELATED DISEASE
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Pred. No. 5
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                                                                                                                    RESULT 15
US-08-860-165-9
                                                                                                                                                                                                                                                                                                            ; MOLECULE TYPE: CDNA
US-08-117-083-7
                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: 415-300 TELEX: 910 277299 INFORMATION FOR SEQ ID NO: 7: SEQUENCE CHARACTERISTICS: FRUGTH: 790 base pairs
                                                                      Sequence 9, Application US/08860165A Patent No. 6004557 GENERAL INFORMATION:
                                                                                                                                                                                                                                                               Query Match
Best Local :
                                                                                                                                                                                                                                                 Matches
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              APPLICANT: EDWARDS, Stirling John
APPLICANT: COX, John Cooper
APPLICANT: WEBB, Elizabeth Ann
APPLICANT: FRAZER, Ian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: Boursn
APPLICANT: Inglis
TITLE OF INVENTION: VARIANTS OF HUMAN PAPILLOMA VIRUS ANTIGENS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
ADDRESSEE: Walter H. Dreger
STREET: 4 Embarcadero Center,
                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION: TELEPHONE: 415-781-1989
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TITLE OF INVENTION: Recombinant Virus
TITLE OF INVENTION: Papilloma Virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES:
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TELEPHONE: 415-398-3249
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                                                                                                                                                                                                                                                                                                                                                    TYPE: nucleic acid
STRANDEDNESS: doub
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CLASSIFICATION: 435
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nes 17; Conserv
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REGISTRATION NUMBER: 24,190
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: A-58783
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                                                                                                                                                                            342 TGTCAAAAGCCACTGTGTCC 361
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344 TGTCAAAAGCCACTGTGTCC 363
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                                                                                                                                                                                                                                                                                                                                          linear
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85.0%;
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0; Mismatches
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Pred. No. 55
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                                                                 Best Local Similarity Matches 17; Conserv
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                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                 FILE REFERENCE: 17227/130
CURRENT APPLICATION NUMBER: US/08/860,165A
CURRENT FILING DATE: 1997-09-22
EARLIER APPLICATION NUMBER: PCT/AU95/00868
EARLIER FILING DATE: 1995-12-20
EARLIER APPLICATION NUMBER: AU PN0157
EARLIER FILING DATE: 1994-12-20
UNMBER OF SEQ ID NOS: 15
                                                                                                                                                                                                                              LENGTH: 801
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                                        NAME/KEY: CDS
LOCATION: (1)..(798)
                                                                                                                                                           OTHER INFORMATION: Description of Artificial Sequence: Gene Fusion
                                                                                                                                                                             FEATURE:
337 TGTCAAAAGCCACTGTGTCC 356
                    1 TGTCAAAAACCGTTGTGTCC 20
                                                                       Conservative
                                                                                     76.0%;
85.0%;
                                                                       0; Mismatches
                                                                                     Score 15.2;
Pred. No. 55;
                                                                                                        DΒ
                                                                                                        Ψ
                                                                                                    Length 801;
                                                                     0,
                                                                     Gaps
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0,

Search completed: August 23, 2003, 12:15:08 Job time : 51 secs